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TITLE

Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G., Horrigan, S., Soppet, D.R. and Weaver, Z.
Cancer gene determination and therapeutic screening using signature

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

REFERENCE AUTHORS	SOURCE	ACCESSI VERSION	RESULT 1 AX329742 LOCUS DEFINITION		45	4.4 4.4 4.4	42	41	39	3.8 '	36	35	c 33	32	30	29	28	26	25.4	23		c 20	19	17	16	14	13	12 1	10	90	7 ء	σ (д . п	·ω	2 ⊦		Result No.	
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Patent: WO 0194629-A 3298 13-DEC-2001;
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/organism="Homo sapiens"
/db_xref="taxon:9606"
_244 c 240 g 227
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Sequence 3393 from Patent WO0229103
AX410746
                                                                                     Alvares,C., Horne,D., Peres-da-Silva,S. and
Gene expression profiles in liver cancer
Patent: WO 0229103-A 3393 11-APR-2002;
GENE LOGIC INC (US)
                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                  2 (bases 1 to 1023)
Schneider, M.C. and Rodriguez, A.
Direct Submission
Submitted (25-APR-1996) M.C. Schneider, Renal Division,
Women's Hospital, 75 Francis Street, Boston, MA 02115, U
                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1023) Rodriguez,A.M., Rodin,D., Nomura,H., Morton,C.C., Weremowicz,S. ar Schneider,M.C.
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Human DNasel-Like III
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VEFKLQSSRAFTNKESYTLRKKTRSKRS"

256 c 249 g 235 t
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protein id="AAH15811."
/db xref="GI:16198311"
/trānslation="MSRELAPLLLLLSIHSALAMRICSFNVRSFGESKQEDKNAMDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clone distribution: MGC clone distribution information can be four through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 38 Row: p Column: 7
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4826697.
Location/Qualifiers
                                                                                             Craniata, Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Julia
                                                                                                                                                                                  Direct Submission Submitted (15-071-2001) National Institutes of Health, Mammalian Submitted (15-071-2001) National Canner
                                                                                                                                                                                                                           Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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contact: amadan@systemsbiology.org
Anup Madan, Rachel Dickhoff, Jessica Fahey, Stephanie Ford,
Greene, Mark Ketteman and Anuradha Madan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 GTAAAACAAAGCTACCTCTACCACGACTATCAGGCTGGAGACGCAGATGTGTTTTCCAGG
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                                                                                                                                                                                                                                                                                                                Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CLONTECH
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 476.8; DB 9;
Pred. No. 1.7e-119;
); Mismatches 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1. :1067
|organism="Homo sapiens"
|db_xref="LocusID:1776"
|db_xref="taxon:9606"
|clone="MGC:27146 IMAGE:4723725"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tissue type="Liver"
|clone lib="NIH MGC 76"
|lab host="DH10B"
                                                                                             Chordata; (Primates; (
         GI:16198370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start=1
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                                                                                           Eukaryota; Metazoa; (
Mammalia; Eutheria; 1
1 (bases 1 to 1067)
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                                                    Homo sapiens.
                                                                                                                                                                  Strausberg, R.
                                                                           Homo sapiens
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                                                                                                                                                                                                      /codon_start=1
/product="NNase1-Like III protein"
/product="NNase1-Like III protein"
/product="104" AAB65957.1"
/db_xref="101:199719"
/translation="MSRELAPLLLLLISIHSALAMRICSFNVRSFGESKQEDKNAMDV
/translation="MSRELAPLLLLLISIHSRIAMRICSFNVRYISSRCGERYKYEDY
AFLYKEKLVSVKRSYHYHDYQDGDADVFSREPFVVWPQSPHTAVKDFVIIPLHTPET
SVKEIDELVEYTDVKRSYHYHDYQDGDADVFSREPFVVWPQSPHTAVKDFVIIPLHTPET
SVKEIDELVEYTYDKRRKARAFIFIRMGDFIVSSVVPKSNSVFDFQKAYKLTEEFALDVSDHFP
VEFKLQSSRAFTNSKKSVTLRKKTKSKRS"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
0
/clone lib="Stratagene liver (#937224)"
/note="corresponds to EST clones 82269 (GenBank Accession Number T68985, T69063), 82738 (GenBank Accession Number T73558, T73655), 78422 (GenBank Accession Number T61400, T61368)"
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/gene="DNAS1L3"
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ilarity 87.8%;
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                                                                                                                                                                                                                                                                               Direct Submission
Submitted (09-FEB-1998) Molecular Biology,
Way, South San Francisco, CA 94080, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                        2 (bases 1 to 1079)
Baron, W.F., Pan, C.Q.,
Baker, K.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo
                                                                                                                                                                                                                                                                                                                                                                                                     Cloning and characterization of an actin-resistant endonuclease secreted by macrophages Gene 215 (2), 291-301 (1998) 98382522
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; (bases 1 to 1079)
Baron, W.F., Pan, C.Q., Spencer, S.A., Ryan, A.M., Lazar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AF047354.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AF047354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sapiens
/translation="MSRELAPLLLLLSIHSALAMRICSFNVRSFGESKQEDKNAMDVIVKVIKRCDIILVMEIKUSNNRICPILMEKLMRNSRRQITYNYVISSRLGRNTYKEQY AFLYKEKLVSVKRSYHYHDYQDGDADVFSREPFVVWFQSPHTAVKDFVIIPLHTTPET SVKEIDELVEVYTDVKHRWARBFIFWGDFNAGCSYVPKKAMKNIRLATDFREVWLIG DQEDTTVKKSTNCAYDRIVLRGQEIVSSVVPKSNSVFDFQKAYKLTEEEALDVSDHFP VEFKLQSSRAFTNSKKSVTLRKKTKSKRS"
                                                                                                /codon_start=1
/product="liver and spleen DNase
/protein id="AAC35752.1"
/db_xref="GI:2905786"
                                                                                                                                                          /note="actin resistant
I; LS-DNase"
                                                                                                                                                                                                                               /db_xref="taxon:9606"
1. .1079
                                                                                                                                                                                       gene="LSD"
                                                                                                                                                                                                                  /gene="LSD"
                                                                                                                                                                                                                                                         organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GI:2905785
                                                                                                                                                                                                   . 988
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                                                                                                                                                                                                                                                                                                                                                         Spencer, S.A.,
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'~en DNase f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 spleen
                                                                                                                                                                     acivity;
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                                                                                                                                                                                                                                                                                                                                                         Ryan, A.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nRNA linear
precursor (LSD)
                                                                                                                                                                     macrophage
                                                                                                                            precursor'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hominidae;
                                                                                                                                                                                                                                                                                                               Genentech
                                                                                                                                                                                                                                                                                                                                                         Lazarus, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lazarus, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                           DNase I-like
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mRNA,
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; Homo.
                                                                                                                                                                     specific
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                                                                                                                                                                                                                                                                                                              Inc.,
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RESULT 8
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AUTHORS
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ORIGIN
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                                                                                    TITLE
      JOURNAL
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Best Local Similarity
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1 (bases 1 to 1108)
Shiokawa,D., Hirai,M. and Tanuma,S.
Shiokawa,D., Hirai,M. and Tanuma,S.
CDNA cloning of human DNase gamma: chromosomal
gene and enzymatic properties of recombinant pr
Apoptosis 3 (2), 89-95 (1998)
2 (bases 1 to 1108)
5 Shiokawa,D. and Tanuma,S.
Direct Submission
Submitted (23-OCT-1996) Biochemistry, Science U
                                                                                                                                                                                                                                                                                                                  CTCGTCTTTGATTTCCAGAAAGCTTACAGGTTGTCTGAATCGAAGGCCCTGG
                                                                                                                                                                                                                                                                                                AGTGTTTTTGACTTCCAGAAAGCTTACAAGCTGACTGAAGAGAGGCCCCTGG
                                                                                                                                                                                                                                                                                                                                                   TATGACAGGATTGTGCTTAGAGGACAAGAAATCGTCAGTTCTGTTGTTCCCAAGTCAAAC
                                                                                                                                                                                                                                                                                                                                                                 TTTGTTTTGGCTGATCGGGGACCAAGAGGACACCACGGTGAAGAAGAAGACCAACTGTGCA
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                                                                                                                                                                                       Homo sapiens
U75744
U75744.1 GI:
                                                                                                                        Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                  Homo sapiens
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/product="liver and spleen DNase"
, 260 c 252 g 237 t
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/evidence=experimental
131. 985
                                                                                                                                                                                                                   DNase gamma mRNA,
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Pred. No. 1.7e-119;
                                                                                                                                                                                                                              1108 bp
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                                                                                                                        Craniata; Vertebrata; I Catarrhini; Hominidae;
                                                                                                                                                                                                                   complete cds.
                                                                                  chromosomal localization
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    Science
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     Univ.
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    of Tokyo,
                                                                                                                                     Euteleostomi;
                                                                                                                                                                                                                               PRI 17-JUN-1998
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FEATURES

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Liu.O.Y., Singh,R.K., Lin,W. and Sikorska,M.
Liu.O.Y., Singh,R.K., Lin,W. and Sikorska,M.
Submitted Submission
Submitted (24-DEC-1997) Institute for Biological Sciences, National
Research Council, 1200 Montreal Road, Bldg. M-54, Box 4, Ottawa, ON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /protein_id="AAC28937.1"
/db_xref="G1:3395772"
/db_xref="G1:3395772"
/tb_sref="G1:3395772"
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VWLIGDGEDTTVKKSTSCAYDRIVLRGGEIVNSVVPRSSGVFDFQKAYELSEEFALDV
SDHFPVBFKLQSSRFATNSRKSVSLKKKKKGSRS"

333 c 320 g 327 t
                                           Craniata, Vertebrata, Buteleostomi,
Sciurognathi, Muridae, Murinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         384 GAGAAGCTGAATGGAAACTCACGAAGAAGCACGACATACAACTACGTGATTAGCTCTCGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /strain="Sprague-Dawley"
/db_xref="taxon:10116"
/tissue_type="liver"
153.
/function="apoptotic endonuclease"
/note="similar to rat DNAse I; chromatin-bound"
                                                                                                                              Lin, W., Ribecco, M.,
LeBlanc, J., Walker, P.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 83;
                                                                                                                                                                                      coding for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 459.2; DB 10,
Pred. No. 1.1e;114;
0; Mismatches 83;
                                                                                                                              Singh, R.K., Lin, W.,
                                                                                                                                                                                      DNaseY: a rat DNaseI-like gene coding fo
expressed chromatin-bound endonuclease
Biochemistry 37 (28), 10134-10143 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Rattus norvegicus"
                                                                                      Liu,Q.Y., Pandey,S., Singh,R.K
Borowy-Borowski,H., Smith,B.,
Sikorska,M.
                   Rattus norvegicus
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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/product="DNAseY"
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86.0%;
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TITLE
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                                                                                                        REFERENCE
                                                                                                                           AUTHORS
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/product="DNase gamma"
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SVKEIDELVEVYTDVKHRWKAENFIEMGDFNAGCSYVPKKAWKNIRLRTDPRFVWLIG
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Shinjuku-ku Ichigaya Funagawaracho, Tokyo 162, Japan
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function="deoxyribonuclease"
                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
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Shiokawa,D. and Tanuma,S.
Molecular cloning and expression
endonuclease DNase gamma
Biochem. J. 332 (Pt 3), 713-720 (
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Shiokawa,D., Ohyama,H.,
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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353 c 333 g 345 t
                                                                                                                                                         /protein_id="AAC40134.1"
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TTPETSVKEIDELADVYTDVRRRWKAENFIFMGDFNAGCSYVPKKAWKNIRLRTDPNF
VMLJEDQEDTTVKKSTSCAYDRIVLRGQEIVNSVVPRSSGVFDFQKAYELSEBEALDV
                                                                                                                                                                                                                                                                                                                                                                 /organism="Rattus norvegicus"
/strain="Sprague-Dawley"
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/product="DNase gamma"
                                                                                                                                                                                                                                                                                                      note="deoxyribonuclease"
                                                                                                                                                                                                                                                                                                                      function="apoptosis"
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GTAAAACAAAGCTACCTCTACCACGACTATCAGGCTGGAGACGCCAGATGTGTTTTCCAGG
                                                 CTTGGAAGAAACACATATAAAGAACAGTATGCCTTTCTCTATAAAGAAAAGCTAGTGTCT
                                                                                   GAGAAGCTGAATGGAAACTCACGAAGAAGCACGACATACAACTACGTGATTAGCTCTCGG
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                                                                                                                                                                                                                                                                                                                                              Sequence 2
AR047845
AR047845.1
                                                                                                                                                                                                                                               Patent: US 5821103-A
                                                                                                                                                                                                                                                                    Tanuma, S.-i
                                                                                                                                                                                                                                                                                                          Unknown
                                                                                                                                                                                                                                                          Deoxyribonuclease
                                                                                                                                                                                                                                                                                                                      Unknown
                                                                                                                                                                                                                                                                                              Unclassified
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                                                                                                                                                                                                 319
                                                                                                                                   Conservative
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                                                                                                                                                                                             organism="unknown"
304 c 283 g
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1. .1208
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                                                                                                                                 Score 452.8; DB 6;
Pred. No. 6.4e-113;
0; Mismatches 87;
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US 5821103
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Mus musculus.

Mus musculus

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Bukaryota; Metazoa; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

I (bases 1 to 941)

Shiokawa, D., Hatanaka, T. and Tanuma, S.

Direct Submission, Dischemistry, Science Univ. of Tokyo,

Shomitted (24-OCT-1996) Biochemistry, Science Univ. of Tokyo,

Shinjuku-ku ichiqaya funagawaracho, Tokyo 162, Japan

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                 243 gagaagcigaarggaaacrcacgaagaagcacgacaracaacracgacrgarragcrcrcgg 302
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                                                                                                                                                                                                                                                                                                                                                                CTTGGAAGAAACACATATAAAGAACAGTATGCCTTTTCTCTATAAAGAAAAGCTAGTGTCT
                                                                                                                                                                                                                                                                                                                                                                                                        303 CTTGGAAGAAACACATATAAAGAACAGTATGCCTTCCTCTACAAGGAGAAGCTGGTGTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 GAACCCTTTGTGGTCTGGTTCCAGTCACCCTACACCCTGTCAAGGACTTCGTGATTGTC
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                                                                                                                                                                                Length 1208;
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Mus musculus DNase gamma mRNA, complete cds.
                                                                                                                                                                           Score 452.8; DB 6;
Pred. No. 6.4e-113;
0; Mismatches 87;
                                                                                                              302
                                            1. .1208
/organism="Rattus rattus"
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/strain="C57 black"
.1208
                                                                                    /db_xref="taxon:10117"
304 c 283 g
                  Location/Qualifiers
                                                                                                                                                                              Ouery Match
Best Local Similarity 85.3%;
Matches 505; Conservative
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VERSION
KEYWORDS
SOURCE
ORGANISM
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AUTHORS
TITLE
                                                                                                              BASE COUNT
ORIGIN
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MMU76110
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/product='Novel deoxynbonuclease(DNase) gamma which cut
specifically linker site of chromatin DNA' FT
86
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C12N9/16, C07K14/47, C07K16/40, C12N1/21, C12N15/09, (C12N1/21,
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GTGAAGGCAAAATACCTCTACCATGACTATCAGGATGGAGACACAGACGTGTTTTCCAGG
                                                                                                                                      ACAGATGTGAAACGTCGCTGGAATGCAGAGAATTTCATTTTCATGGGTGACTTCAATGCT
                                            GAACCCTTTGTGGTCTGGTTCCAGTCACCCTACACGCTGTCAAGGACTTCGTGATTGTC
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/tissue_type='Thymus, Spleen'
nucleus'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent: JP 1996187079-A 1 23-JUL-1996;
TANUMA YASUKAZU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-SEP-1995 JP 1995255647
06-SEP-1994 JP 94P 239518
TANUMA YASUKAZU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           strandedness: Double;
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JP 1996187079-A/1
23-JUL-1996
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hypothetical: No;
anti-sense: No;
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5'UTR
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JP 1996187079-A/1.
Rattus rattus.
Rattus rattus
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CC STRAIN
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E11687
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AUTHORS
TITLE
JOURNAL
       363
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KEYWORDS
SOURCE
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ROD 26-JAN-1999

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ACCESSION
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACGGATGTGAGAAGCCAGTGGAAGACAGAGAATTTCATCTTCATGGGTGATTTCAACGCC
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 Mus musculus
Eukaryota; M
                             Mus musculus.
                                                           AF047355.1
                                                                                                  Mus musculus
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229 c 228 g 229 t
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/protein_id="AAD09222.1"
/db_xref="GI:4098208"
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Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                           GI:2905787
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83.4%;
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Pred. No. 4.1e-108;
Pred. No. 4.1e-108;
                                                                                                  1124 )
spleen
                                                                                                  n DNase
                                                                                                               mRNA
                                                                                                  precursor
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sor (LSD)
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GTGAAGACAAAATACCACTACCATGACTATCAGGATGGAGACACAGACGTGTTTTCCAGG
                                                                                                                                                                                                                                                                                       CTTGGAAGAAACACGTACAAAGAGCAGTATGCCTTCGTCTACAAGGAGGAGAAGCTGGTGTCT
                                                      ACAGATGTGAAACGTCGCTGGAATGCAGAGAATTTCATTTTCATGGGTGACTTCAATGCT
                                                                                                               GAGCCCTTTGTGGTTTGGTTCCATTCCCCCTTTACTGCTGAAGGACTTCGTGATTGTC
                                                                                                                                                                                                                                                                                                                     CTTGGAAGAACACATATAAAGAACAGTATGCCTTTCTCTATAAAGAAAAGCTAGTGTCT
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                                 ACGGATGTGAGAAGCCAGTGGAAGACAGAGAATTTCATCTTCATGGGTGATTTCAACGCC
                                                                                             494;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (09-FEB-1998) Molecular Biology, Way, South San Francisco, CA 94080, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cloning and characterization of an actin-resistant endonuclease secreted by macrophages Gene 215 (2), 291-301 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 1124)
Baron, W.F., Pan, C.Q., Spencer, S.A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 (bases 1 to 1124)
Baron,W.F., Pan,C.Q., Spencer,S.A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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248. .1102
/gene="LSD"
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173. .1105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="liver and spleen DNase"
273 c 273 g 279 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTPETSVKE I DELVDVYTDVRSQWKTENF I FMGDFNAGCSYVPKKAWQN I RLRTDPKF
VWL I GDQEDTTVKKSTSCAYDR I VLCGQE I VNSVVPRSSGVFDFQKAYDLSEEEALDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /trānslation="MSLHPASPRLASLLLFILALHDTLALRLCSFNVRSFGASKKENH
EAMDIIVKIIKRCDLILLMEIKDSSNNICPMLMEKLNGNSRRSTTYNYVISSRLGRNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Mus musculus"
/db_xref="taxon:10090"
1. .1124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'gene="LSD"
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/product="liver and spleen
/protein_id="AAC35753.1"
/db_xref="GI:2905788"
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                                                                                                                                                                                                                                                                                                                                                                                                                  Score 435.2; DB 10;
Pred. No. 4.1e-108;
0; Mismatches 98;
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EAMDI IVKI IKRCDLILLMBIKDSSNNICPMLMBKLAGNSKESTIVNVISSRLGRNT
YRRQYAFVYKEKLVSVWTKYNYHDYDGOGDTDVFSREPFVVWFHSPFTAVKDFVIVPLH
YTTPFTSVKEIDBLUDVYTDVKSQWKTENFIPKOPFNAGCSYVPKKAMQNIRLRTDPKF
WLIGDQEDTTVKKSTSCAYDRIVLCGQEIVNSVVPRSSGVFDFQKAYDLSEEBALDV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Clone distribution: MGC clone distribution information can be foun through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 18 Row: i Column: 14 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 6681204.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (15-MUG-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Anuradha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tissue type="Liver." ormal. 5 month old male mouse." (clone Tib="NCI CGAP_Li9" lab_host="DH10B"
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                                                       480
                                                                                             883
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Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbiology.org
contact: amadan@systemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anurad
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
                                                                                                                                 TATGACAGGATTGTGCTTTGTGGACAAAGAGATAGTCAACTCCGTGGTTCCCCGTTCCAGT
                                                                                                                                                                                                                                                                                                                                     Mus musculus, Similar to deoxyribonuclease 1-like 3, clone MCC:13854 IMAGE:4160709, mRNA, complete cds.
               gecreraderaceccaagaaggecregeagaacarregrrigaggacggacccaag
                                                                                           rrrgrrrggcrgarrggggccaagaggacacracggrcaagaagagraccagcrgrgcc
                                                       TTCGTTTGGCTGATCGGGGACCAAGAGGACACCACGGTCAAGAAGAGACACAAAACTGCGCC
product="Similar to deoxyribonuclease 1-like 3"
                                                                                                                                                                                                                                   CTCGTCTTTGATTTCCAGAAAGCTTACAGGTTGTCTGAATCGAAGGCCCTGG 592
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'db_xref="GI:15215119"
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VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                    DEFINITION
                                                                                                                                                                                                                                                                                                             RESULT 15
BC012671
LOCUS
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AUTHORS
TITLE
JOURNAL
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Pred. No. 1.2e-
0; Mismatches
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Job time : 1260.59 secs
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Result
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Searched:
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ALIGNMENTS

RESULT 1 AAD29088

AAD29088 standard; cDNA; 592

ВP

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Cbs
                                                                                                                                                                                                  Bovine; fertility associated antigen; FAA; sperm fertility; acrosome; artificial insemination; plasma membrane; sperm cell; anti-infertility; reproductive tract; ss.
                   14-JUL-2000; 2000US-218140P
                                        16-JUL-2001; 2001WO-US22097.
                                                                                                                                                                               Bos sp.
                                                                                                                                                                                                                                          Bovine fertility associated antigen (FAA) partial cDNA
                                                                                                                                                                                                                                                                 16-MAY-2002
                                                                                                                                                                                                                                                                                      AAD29088;
(ARIZ-) ARIZONA BOARD OF REGENTS.
                                                             24-JAN-2002.
                                                                                  WO200206444-A2
                                                                                                                                                                                                                                                               (first entry)
                                                                                                          /*tag= a
/product= "Bovine fertility associated antigen (FAA)"
/note= "CDS does not include start and stop codon"
                                                                                                                                                          Location/Qualifiers
                                                                                                       partial)
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The invention relates to bovine fertility associated antigen (FAA) and its nucleic acid sequence. FAA is useful for increasing the stability of the plasma membrane plus acrosome of a sperm cell and/or other portions of a sperm cell, in particular mammalian sperm cell such as a sperm cell from buffalo, cow, horse, mice, pig, sheep, human, avian sperm cell from cell such as a sperm cell including turkey or chicken sperm cell. FAA is also useful for increasing the fertility of sperm from a mammal including buffalo, cow, horse, mice, pig, sheep or human, or avian (chicken or turkey). FAA is added to the suspension of sperm cells prior to preservation or prior to administration of the sperm cells to a mammal in artificial insemination. Alternatively, fertility of sperm from a mammal is increased by placing FAA into a female's reproductive tract prior to deposition of the sperm cells insemination. The female mammal is increased by injecting insemination. The female mammal is increased by injecting FAA into the male mammal's reproductive tract. The present sequence is Novel amino acid and polynucleotide sequence for fertility associated antigen useful for increasing stability of plasma membrane, acrosome and other portions of sperm cell, and increasing fertility of mammals Claim 1; Fig 6; 37pp; English. Bellin ME 2002-171803/22 RL, P-PSDB; AAE18281 Ķ Ï Zhang

Sequence 592 BP; 170 A; 143 C; 142 G; 137 T; 0 other;

bovine fertility associated antigen (FAA) partial cDNA

Gaps 0, DB 24; Length Indels . 0 .0%; Score 592; DB 24 .0%; Pred. No. 6e-178; Mismatches .; 0 100.08; Conservative Similarity Local Simi hes 592; Query Match

120 9 GAGAAGCTAAAACGGAAATTCAAGAAAAGGCATAACATACAACTATGTGATTAGCTCTCGC **CTTGGAAGAAACACATATAAAGAACAGTATGCCTTTCTCTATAAAGAAAAGCTAGTGTCT** GAGAAGCTAAACGGAAATTCAAGAAAAGGCATAACATACAACTATGTGATTAGCTCTCGC 61 a ò ò

GTAAAACAAAGCTACCTCTACCACGACTATCAGGCTGGAGACGCAGATGTGTTTTCCAGG GTAAAACAAAGCTACCTCTACCACGACTATCAGGCTGGAGACGACGATGTGTTTTCCAGG 121 121

CTTGGAAGAAACACATATAAAGAACAGTATGCCTTTCTTATAAAGAAAAGCTAGTCT

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GAACCCTTTGTGGTCTGGTTCCAGTCACCCTACACGCTGTCAAGGACTTCGTGATTGTC GAACCCTTTGTGGTCTGGTTCCAGTCACCCTACACCGCTGTCAAGGACTTCGTGATTGTC 181 181

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481

CTCGTCTTTGATTTCCAGAAAGCTTACAGGTTGTTGTATTGAATCGGAGGCCCTGG 541 g

592

AAD29089

671 DNA; AAD29089 standard;

BP.

AAD29089;

(first entry) 16-MAY-2002

coding sequence. (rFAA) recombinant FAA Bovine 22kDa

Bovine, fertility associated antigen, FAA, sperm fertility, acrosome, artificial insemination, plasma membrane, sperm cell, anti-infertility, reproductive tract; ds.

Bos sp

WO200206444-A2.

24-JAN-2002.

16-JUL-2001; 2001WO-US22097.

14-JUL-2000;

(ARIZ-) ARIZONA BOARD OF REGENTS.

Bellin ME; Zhang H, Ax RL,

WPI; 2002-171803/22.

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Novel amino acid and polynucleotide sequence for fertility associated antigen useful for increasing stability of plasma membrane, acrosome and other portions of sperm cell, and increasing fertility of mammals

Claim 1; Fig 5; 37pp; English.

The invention relates to bovine fertility associated antigen (FAA) and its nucleic acid sequence. FAA is useful for increasing the stability of the plasma membrane plus acrosome of a sperm cell and/or other portions of a sperm cell, in particular mammalian sperm cell such as a sperm cell including turkey or chicken sperm cell. FAA is also useful for increasing the fertility of sperm from a mammal including buffalo, cow, horse, mice, pig, sheep or human, or avian (chicken or turkey). FAA is added to the suspension of sperm cells prior to preservation or prior to amice, pig, sheep or human, or avian (chicken or turkey). FAA is added to the suspension of sperm cells for a mammal in artificial insemination. Alternatively, fertility of sperm from a mammal is increased by placing calls into the female's reproductive tract prior to deposition of the sperm cells into the female's reproductive tract by copulation or artificial insemination. The fertility of the male mammal is increased by injecting the insemination. The fertility of the male mammal is increased by injecting the male mammal's reproductive tract. The present sequence is bovine 22kDa recombinant FAA (rFAA) coding sequence.

Sequence 671 BP; 195 A; 166 C; 154 G; 156 T; 0 other;

Gaps ö 671; 100.0%; Score 592; DB 24; Length 100.0%; Pred. No. 6.5e-178; Indels . 0; Mismatches Conservative Local Similarity 592; Query Match

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9 98 27 GAGAAGCTAAACGGAAATTCAAGAAAAGGCATAACATACAACTATGTGATTAGCTCTCGC 1 GAGAAGCTAAACGGAAATTCAAGAAAAGGCATAACATACAACTATGTGATTAGCTCTCGC 셤

120 CTTGGAAGAAACACATATAAAGAACAGTATGCCTTTCTCTATAAAGAAAAGCTAGTGTCT 146 CTTGGAAGAAACACATATAAAGAACAGTATGCCTTTCTCTATAAAGAAAAGCTAGTGTCT 61 ð 셤

121 GTAAAACAAAGCTACCTCTACCACGACTATCAGGCTGGAGACGCAGATGTGTTTTCCAGG 180 ò

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(ZHAN/)
(AXRL/)
                            07-APR-2000; 2000US-195225P
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                                              09-APR-2001; 2001WO-US10802
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AX R L.
                                                                                                                                                                                                                                                                                                              bovine fertility-associated antigen (FAA).
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                                                                                                    /transl except= (pos:325..326, aa:R)
/note= "This codon has an appent 1 nucleo
deletion which alters the reading f
/transl_except= (pos:576..578, aa:RLSESKAL)
                                                                                                                                                                                       /*tag= a
/product= "FAA"
/note= "Fertility-associated antigen"
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antigen (FAA) and a bovine FAA polypeptide. Human or bovine FAA is useful CC for increasing the stability of a sperm cell acrosome and for increasing the fertility of a human male by administering FAA. Detecting single cc the fertility of a human male by administering FAA. Detecting single nucleotide polymorphisms (SNPs) of the human or bovine FAA gene is useful for assaying fertility by detecting the presence or absence of a FAA SNP CC in the mammal and correlating the presence or absence with the fertility of the mammal. The FAA SNPs are chosen from FAA SNPs 1-34 given in the CC fitness of a human or bovine, by determining the reproductive fitness of a human or bovine, by determining the nucleotide sequence of the FAA SNP and correlating the frequency of the FAA SNP to the reproductive fitness of the mammals. FAA improves the integrity of sperm combranes and increases the capacitation of sperm derived from either fertile or infertile humans. Early genetic identification of infertility improves the prognosis for subsequent attempts at fertilisation and CC facilitates early intervention to determine whether the individual may benefit from fertility treatments to avoid costly and/or emotional containing containing the costly and/or emotional containing containing the first for subsequent attempts at fertilisation and containing the fertility treatments to avoid costly and/or emotional containing the first for subsequent attempts at fertility associated antigen (FAA) described in the method of the
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Sequence 578 BP; 167 A; 140 C; 138 G; 133 T; 0 other;

Query Match
Best Local Simi
Matches 569; Similarity Conservative 91.0**%**; 98.3**%**; Score 539; DB 24; Length 578; Pred. No. 4.4e-161; O; Mismatches O; Indels 1 10; Gaps <u>ب</u>

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AACTGCGCCTATGACAGGATCGTGCTTAGAGGACAAAATATTGTCAACTCTGGTGGTCCT
                                                                GACCCCAAGTTCGTTTGGCTGATCGGGGGACCAAGAGGACACCACCGCTCAAGAAGAGCACA 471
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                                                                                                                                                                                                                                            Fertility-associated antigen; FAA; antiinfertility; sperm cell acrosome; reproductive fitness; single nucleotide polymorphism; SNP; human;
480 AACTGCGCCTATGACAGGATCGTGCTTAGAGGACAAAATATTGTCAACTCTGGTGGTCCT 539
                                                                                                                                                                                                                 Partail cDNA encoding human fertility-associated antigen (FAA), HC1
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                                                                                                                                                                                                                                                                                                                                                                                                     partial
factor No start or stop codon given.
Lransl_except= (pos:1..3, aa:KVIKRCDIILVMEIKDS)
fransl_except= (pos: 253..255, aa:S)
                                                                                                                                                                                                                                                                                                                                                                                           note= "Human fertility-associated antigen,
                                            540 CAATCAAACCTCGTCTTTGATTTCCAGAAAGCTTACAGG 578
                            532 CAATCAAACCTCGTCTTTGATTTCCAGAAAGCTTACAGG 570
                                                                                                                                                                                                                                                                                                                                                                            "Human FAA"
                                                                                                                                                                                                                                                                                                                                  location/Qualifiers
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                                                                                                                             AAS17901 standard; cDNA; 556
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                                                                                                                 Length 556;
fertility-associated antigen (FAA), HC1, one of 4 partial clones of the novel FAA gene described in the method of th
                                                                                                        Score 492.4; DB 24; Length
Pred. No. 3e-146;
0; Mismatches 21; Indels
                                                                Sequence 556 BP; 159 A; 130 C; 142 G; 125 T; 0 other;
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                                                                                                            83.2%;
96.0%;
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                                                                                                                                                    Matches 505;
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Claim

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The invention relates to a novel method for diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma or metastatic liver curve tumour in a patient, and differentiating metastatic liver cancer from hepatocellular carcinoma in a patient, involving detecting the level of expression of two or more genes represented in ABN93503-ABN97455 in a tissue sample. The method of the invention has hepatotropic, and cycostatic activity. The method is useful for diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma and metastatic liver carcinoma in a patient. The method is useful for identifying expression profiles which serve as useful diagnostic markers as well as markers that can be used to monitor disease states, disease progression, drug toxicity, drug efficacy and drug metabolism.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at fifth the proposition of the published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local S
Matches 520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1023 BP; 312 A; 244 C; 240 G; 227 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma or metastatic liver tumor in a patient, involves detecting the level of expression of two or more genes in liver tissue sample
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GAGAAGCTAAACGGAAATTCAAGAAAAGGCATAACATACAACTATGTGATTAGCTCTCGC
                                                                                                                  TTCGTTTGGCTGATCGGGGACCAAGAGGACACCACCGGTCAAGAAGAGAGACACAAACTGCGCC
                                                                                                                                                                                                                                         GAACCCTTTGTGGTCTGGTTCCAGTCACCCTACACCGCTGTCAAGGACTTCGTGATTGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTTGGAAGAAACACATATAAAGAACAATATGCCTTTCTCTACAAGGAAAAGCTGGTGTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTTGGAAGAAACACATATAAAGAACAGTATGCCTTTCTCTATAAAGAAAAGCTAGTGTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAGAAGCTGAACAGAAATTCAAGGAGAGGCATAACGTACAACTATGTGATTAGCTCTCGG
                                AGTGTTTTTGACTTCCAGAAAGCTTACAAGCTGACTGAAGAGGAGGCCCTGG
                                                             CTCGTCTTTGATTTCCAGAAAGCTTACAGGTTGTCTGAATCGAAGGCCCTGG 592
                                                                                            TATGACAGGATTGTGCTTAGAGGACAAGAAATCGTCAGTTCTGTTGTTCCCAAGTCAAAC
                                                                                                                                                       TTTGTTTGGCTGATCGGGGACCAAGAGGACACCACGGTGAAGAAGAGCACCAACTGTGCA
                                                                                                                                                                                                                       GGCTGCAGCTACGTCCCCAAGAAGGCCTGGAAGAACATCCGCTTGAGGACTGACCCCAGG
                                                                                                                                                                                                                                                                                 ACGGACGTGAAACACCGCTGGAAGGCGGAGAATTTCATTTCATGGGTGACTTCAATGCC
                                                                                                                                                                                                                                                                                                     ACAGATGTGAAACGTCGCTGGAATGCAGAGAATTTCATTTCATGGGTGACTTCAATGCT
                                                                                                                                                                                                                                                                                                                                                                     GAGCCCTTTGTGGTCTGGTTCCAATCTCCCCACACTGCTGTCAAAGACTTCGTGATTATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTGAAGAGGAGTTATCACTACCATGACTATCAGGATGGAGACGCAGATGTGTTTTCCAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTAAAACAAAGCTACCTCTACCACGACTATCAGGCTGGAGACGCAGATGTGTTTTCCAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               80.5%;
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0; Mismatches
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Young P
Soppet
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20-SEP-2000; 2000US-23405P

20-SEP-2000; 2000US-234557P

22-SEP-2000; 2000US-23452P

25-SEP-2000; 2000US-235007P

25-SEP-2000; 2000US-23503P

25-SEP-2000; 2000US-235380P

25-SEP-2000; 2000US-23538P

25-SEP-2000; 2000US-2353P

25-SEP-2000; 2000US-2353P

26-SEP-2000; 2000US-2353P

27-SEP-2000; 2000US-2353P

27-SEP-2000; 2000US-23571P

27-SEP-2000; 2000US-23563P

28-SEP-2000; 2000US-23563P

28-SEP-2000; 2000US-23563P

28-SEP-2000; 2000US-23563P

28-SEP-2000; 2000US-23563P

28-SEP-2000; 2000US-23561P

28-SEP-2000; 2000US-23663P

28-SEP-2000; 2000US-23663P

28-SEP-2000; 2000US-23663P

28-SEP-2000; 2000US-23661P

29-SEP-2000; 2000US-23661P

29-SEP-2000; 2000US-23611P

29-SEP-2000; 2000US-23611P

29-SEP-2000; 2000US-237778P

02-CCT-2000; 2000US-237729P

02-CCT-2000; 2000US-237729P

02-CCT-2000; 2000US-23773P

02-CCT-2000; 2000US-23773P

02-CCT-2000; 2000US-23779P

03-CCT-2000; 2000US-23790P

03-CCT-2000; 2000US-23790P

03-CCT-2000; 2000US-23790P

03-CCT-2000; 2000US-23760P

03-CCT-2000; 2000US-23760P
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18-SEP-2000;
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                                                                                                           (AVAL-) AVALON PHARM
Augustus M, Weaver Z;
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                                 Horrigan
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Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid; stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous; cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;

Homo sapiens

gene; ds.

Stomach cancer related gene sequence SEQ ID NO:2795.

(first entry)

15-MAY-2002

BP

ABL64458 standard; DNA; 1023

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The present invention describes a method (M1) for screening for an anti-neoplastic agent. The method involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, determining a change in expression of at least one gene (I) of a signature gene set, where (I) comprises a sequence (S) selected from 8447 sequences (given in ABL61664 to ABL70110), or is at least 95% identical to (S), where a change in expression is indicative of anti-neoplastic activity, (I) has cytostatic activity and can be used in gene therapy. MI can be used for screening an anti-neoplastic agent, and can be used for producing a product which is the data collected with respect to the anti-neoplastic agent as a result of M1, and the data is sufficient to convey the chemical structure and/or properties of the agent. M1 can be used in the treatment of cancer such as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney, prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine
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Screening for anti-neoplastic agent involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, and determining a change in expression of a gene of a signature gene set
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Pred. No. 3.8e-141;
); Mismatches 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   carcinoma, papillary carcinoma and Wilm's tumour.
                                                                                                                                Claim 1; SEQ ID 251; 44pp; English
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87.8%;
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Horrigan S;
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2000US-233133P,
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2000US-234923P.
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2000US-235638P.
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03-OCT-2000; 2000US-237606P.
03-OCT-2000; 2000US-237608P.
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2000US-236028P
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                                                                                                              WO200194629-A2.
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20-SEP-2000;
20-SEP-2000;
20-SEP-2000;
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02-OCT-2000;
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25-SEP-2000;
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02-OCT-2000;
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Soppet DR,
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TTCGTTTGGCTGATCGGGGACCAAGAGGACACCACGGTCAAGAAGAGCACAAAACTGCGCC 480

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TATGACAGGATTGTGCTTAGAGGACAAGAAATCGTCAGTTCTGTTGTTCCCAAGTCAAAC

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781 AGTGTTTTTGACTTCCAGAAAGCTTACAAGCTGACTGAAGAGGAGGCCCTGG 832 CTCGTCTTTGATTTCCAGAAAGCTTACAGGTTGTCTGAATCGAAGGCCCTGG

RESULT 7 ABL64458

determining a change

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes a method (M1) for screening for an anti-neoplastic agent. The method involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, determining a change in expression of at least one gene (I) of a signature gene set, where (I) comprises a sequence (S) selected from 8447 sequences (given in ABL61664 to ABL70110), or is at least 95% identical to (S), where a change in expression is indicative of anti-neoplastic activity. (I) has cytostatic
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Screening for anti-neoplastic agent involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, and determining a change in expression of a gene of a signature gene

Augustus Weaver 2

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20-SEP-2000

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29-SEP-2000

20-CT-2000

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03-CCT-2000

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03-CCT-2000
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                                                                                        (AVAL-)
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2000US-233617P.
2000US-234009P.
2000US-234009P.
2000US-234509P.
2000US-234509P.
2000US-234924P.
2000US-234924P.
2000US-235077P.
2000US-235087P.
2000US-235087P.
2000US-235637P.
2000US-235637P.
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2000US-235637P.
2000US-23563P.
2000US-23603P.
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2000US-23603P.
2000US-236111P.
2000US-236109P.
2000US-236111P.
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Query Match
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Matches 520; (
The present invention describes a method (MI) for screening for an anti-neoplastic agent. The method involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, determining a change in expression of at least one gene (I) of a signature gene set, where (I) comprises a sequence (S) selected from 8447 sequences (given in ABL61664 to ABL70110), or is at least 95% identical to (S), where a change in corpusion is indicative of anti-neoplastic activity. (I) has cytostatic activity and can be used in gene therapy. MI can be used for screening an anti-neoplastic agent, and can be used for producing a product which is the data collected with respect to the anti-neoplastic agent as a result of MI, and the data is sufficient to convey the chemical result as colon, breast, stomach, lung, thyroid, cosophageal, ovarian, kidney, prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell carcinoma, neuroendocrine infiltrating ductal cancer, stement.
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Pred. No. 3.8e-141;
0; Mismatches 72;
SEQ ID 3298; 44pp; English.
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Matches 520; Conservative
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This DNA sequence encodes a novel human LS-DNase (AAW23542), which has DNA-hydrolytic activity but is resistant to inhibition by actin. It can be used for reducing the viscoelasticity or viscous consistency of be used for reducing the viscoelasticity or viscous consistency of DNA-containing material, as well as treatment of systemic lupus erythematosus or pulmonary disease of disorders such as cystic fibrosis, bronchitis, pneumonial, bronchiectasis, emphysema, asthma, tuberculosis or fungal infections. It can also be used for adjunctive treatment of abscesses or severe closed-space infections in conditions such as certaininglis, peritorialis, sinusitis, otilis, peritodontis, peritorialis, cholelithiasis, endocarditis and serior arthritis as well as in topical treatments in a variety of inflammatory and infected lesions, erg. of the skin and mucosal commentanes, surgical wounds, ulcerative lesions and burns. LS-DNase may improve the efficacy of antibiotics used in the treatment of such infing to intext DNA). It can also be used for the treatment of other con-infected conditions in which there is an accumulation of cellular cubulo-interstital kidney disease. It can also be used in in vitro diagnostic assays of a viscous material (e.g. sputum) from a patient.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nostic assays of a viscous material (e.g. sputum) from a patient. anti-LS-DNase antibodies can be used for detection and purification
                                                                       DNase; actin; DNA viscoelasticity; systemic lupus erythematosus; cystic fibrosis; meningitis; pulmonary disease; gene therapy; recombinant preparation; DNA-hydrolytic activity; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated LS-DNase which is resistant to inhibition by a used for the treatment of e.g systemic lupus erythematosus pulmonary diseases and disorders such as cystic fibrosis
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71..988
Human LS-DNase nucleotide sequence.
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/product= LS-DNase
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71..130
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131..985
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P-PSDB; AAW23542.
                                                                                                                                                                                                                                 Homo sapiens
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Gaps

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Length 1079;

Score 476.8; DB 18; Length Pred. No. 3.9e-141; 0; Mismatches 72; Indels

80.5%; ilarity 87.8%; Conservative

Similarity

GAGAAGCTGAACAGAAATTCAAGGAAGGCATAAACGTACAACTATGTGATTAGCTCTCGG 346

287 Н

셤 ò

AAT74076 standard; cDNA; 1079

RESULT 9 AAT74076 AAT74076;

GAGAAGCTAAACGGAAATTCAAGAAAAGGCATAACATACAACTATGTGATTAGCTCTCGC

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ABK84429
ID ABK84
XX ABK84
XX ABK84
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XX ABK84
XX Human
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XX Human
XX Freum
XX Freum
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                                                                                                                                                                                                                                               viral infection; parasitic infection; protozoal infection; fungal infection; sterile inflammatory disease; psoriasis; rheumatoid arthritis; glomerulonephritis; asthma; thrombosis; cardiac reperfusion injury; renal reperfusion injury; ARDS; adult respiratory diserses syndrome; inflammatory bowel disease; Crohn's disease; ulcerative colitis; periodontal disease; granulocyte activation; chronic inflammation; allergy.
                           WPI; 2002-435328/46
                                                                                                                                                                                                                                                                                                                                              Human; ss; granulocytic cell; DNA chip; bacterial infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                  ABK84429
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABK84429 standard;
                                                     Beazer-Barclay Y,
                                                                                                            03-OCT-2000; 2000US-237189P
                                                                                                                                    03-OCT-2001; 2001WO-US30821
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                                                                                LOGIC INC.
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Claim 1;
                                                                                                                                                  of genes associated with granulocyte activation, which serves as diagnostic markers that is useful for monitoring disease states and
                                                                                                                                        ID No 1000; 114pp; English
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CC GC, where differential expression of Gs is indicative of GCA.
Also included are modulating (M2) GA by contacting GC with an agent
CC that alters the expression of it least one gene in Gs; (2) screening (M3)
CC chronic) in a tissue, an allergic response in a subject, exposure of a
CS subject to a pathogen or sterile inflammatory disease using the
CC chronic) in a tissue, an allergic response in a subject, exposure of a
CC subject to a pathogen or sterile inflammatory disease using the
CC chronic) in a tissue, an allergic response in a subject, exposure of a
CC subject to a pathogen or sterile inflammatory disease, by detecting the
CC level of expression in a sample of the tissue of gene(s) from Gs, where
CC the level of expression of the gene is indicative of inflammation;
CC (4) treating (M5) an inflammation (especially chronic) or in a tissue,
CC an allergic response in a subject, exposure of a subject to a pathogen
CC inflammation with an agent that modulates the expression of gene(s)
CC from Gs in the tissue. M1 is useful for detecting a firsue having
CC from Gs in the tissue. M1 is useful for detecting an agent capable of modulating
CC detecting an inflammation (especially chronic) in a tissue, an allergic
CC response in a subject, exposure of a subject to a pathogen or sterile
CC inflammatory disease (e.g. psoriasis, rheumatoid arthritis,
CC parasitic infection, protozoal infection, fungal infection and M5 is
CC useful for treating one of the above conditions. The present
CC useful for treating one of the above conditions. The present
CC the printed specification, but was obtained in electronic
CC format directly from Wipo at
CC format directly from Wipo at The invention relates to detecting (M1) granulocyte (GC) activation (GCA), by detecting the level of expression of gene(s) (Gs) identified DNA chip analysis as given in the specification, and comparing the expression level to an expression level in an unactivated ftp.wipo.int/pub/published_pct_sequences λq

Sequence 1108 BP; 329 A; 261 C; 271 G; 247 T; 0 other;

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                      ACAGATGTGAAACGTCGCTGGAATGCAGAGAATTTCATTTCATGGGTGACTTCAATGCT
                                                                GAGCCCTTTGTGGTCTGGTTCCAATCTCCCCACACTGCTGTCAAAGACTTCGTGATTATC
                                                                                                               GAACCCTTTGTGGTCTGGTTCCAGTCACCCTACACCGCTGTCAAGGACTTCGTGATTGTC
                                                                                                                                                  GTGAAGAGGAGTTATCACTACCATGACTATCAGGATGGAGACGCAGATGTTTTTCCAGG
                                                                                                                                                                GTAAAACAAAGCTACCTCTACCACGACTATCAGGCTGGAGACGCAGATGTGTTTTTCCAGG
                                                                                                                                                                                                 CTTGGAAGAAAAACATATAAAGAACAATATGCCTTTCTCTACAAGGAAAAGCTGGTGTCT
                                                                                                                                                                                                               CTTGGAAGAAACACATATAAAGAACAGTATGCCTTTCTCTATAAAGAAAAGCTAGTGTCT
                                                                                                                                                                                                                                                   GAGAAGCTGAACAGAAATTCAAGGAGGGCATAACGTACAACTATGTGATTAGCTCTCGG
                                                                                                                                                                                                                                                                          GAGAAGCTAAACGGAAATTCAAGAAAAAGGCATAACATACAACTATGTGATTAGCTCTCGC 60
                                                                                                                                                                                                                                                                                                    519;
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Pred. No. 1.3
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Detecting granulocyte activation by detecting differential expression

us-09-905-114-1.rng

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Sequence 1208 BP; 319 A; 304 C; 282 G; 303 T; 0 other;
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                                                                                                               rargacadgarrerectragaceacaagaaarcereagrerererectearereaageaaae 848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNase which selectively cuts linker region of chromatin DNA -useful in diagnosis, treatment and prevention of cancer, autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence encodes the deoxyribonuclease, DNase-gammma, which is able to selectively cleave the linker part of chromatin DNA. DNase-gamma has a mol. wt. of 32000 by SDS-PAGE, or 30000 by gel filtration, an optimum H of 5.6, is found in the cell nucleus, is not dependent on divalent cations, has a Zn(2+) inhibition IC(50) > 1mM and leaves 3'-OH and 5'-P termini after cleavage. The DNase can be used at a mol. leval to resolve the control mechanisms of carcinogenesis, the autoimmune system and AIDS development. It can also be used in the diagnosis, prevention and treatment of cancer, autoimmune disease, viral infections, etc.,
               GCCTGCAGCTACGTCCCCCAAGAAGGCCTGGAAGAACATCCGCTTGAGGACTGACCCCAGG
                                                                  TTCGTTTGGCTGATCGGGGACCAAGAGACACCACGGTCAAGAAGAGACACAAACTGCGCC
                                                                                          Deoxyribonuclease; DNase-gammma; selective cleavage; linker; chromatin DNA; cell nucleus; 3'-hydroxy; 5'-phosphate; apoptosis; carcinogenesis; AIDS development; diagnosis; prevention; treatment; cancer; autoimmune disease; viral infections; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                 GAT codon comprising bases 837-839 has no corresponding amino acid in AAR94021"
                                                                                                                                                              849 AGTGTTTTTGACTTCCAGAAAGCTTACAAGCTGACTGAAGAGGAGGCCCTGG 900
                                                                                                                                       CTCGTCTTTGATTTCCAGAAAGCTTACAGGTTGTCTGAATCGAAGGCCCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 4; Pages 55-57; 75pp; Japanese.
                                                                                                                                                                                                                                                                                          Deoxyribonuclease, DNase-gamma cDNA.
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12..944
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/note= "GAT
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                                       Gaps
                                                                                                243 GAGAAGCTGAATGGAAAACTCACGAAGAAGCACGACATACAACTACGTGTTAGCTCTCGG
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                                                                                                                                                  303 CITGGAAGAAACACATATAAAAGAACAGTATGCCTTCCTCTACAAGGAGAAGCTGGTGTCT
                                                                                                                                                                                                                             GTAAAACAAAGCTACCTCTACCACGACTATCAGGCTGGAGACGCAGATGTGTTTTCCAGG
                                                                                                                                                                                                                                                          363 GTGAAGGCAAAATACCTCTACCAIGACTATCAGGATGGAGACACAGACGTGTTTTCCAGG
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 Length 1208;
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                                   Indels
Score 451.2; DB 17;
Pred. No. 5.8e-133;
                                       88;
                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Murine LS-DNase nucleotide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
173..1105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag= c
/product= LS-DNase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /*tag= b
/note= "putative"
248..1105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAT74083 standard; cDNA; 1124
76.2%;
85.1%;
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173..247
                                     Conservative
                 Best Local Similarity
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                                   Matches 504;
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 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This DNA sequence encodes a variant LS-DNase, which has DNA-hydrolytic CC activity but is resistant to inhibition by actin. A 649 base pair CC dragment of the coding sequence of cloned human LS-DNase (ART74076) was used to screen a murine liver cDNA library and obtain this nucleotide. CC Murine mature LS-DNase is 84% identical to human LS-DNase. A portion of the present sequence was used in Northern blot assays of various murine CC tissues. Expression of murine LS-DNase mRNA was found to be highest in CC the liver and spleen. Human LS-DNase and be used for reducing the CC viscoelasticity or viscous consistency of DNA-containing material, as CC well as treatment of systemic lupus exythematosus or pulmonary disease CC disorders such as cystic fibrosis. It can also be used for adjunctive treatment of abscesses or severe closed-space infections, e.g. CC meningitis. It may improve the efficacy of antibiotics used in the CC treatment of such infections (e.g. gentamicin activity is markedly creduced by reversible binding to intact DNA). It can also be used in in CC vitro diagnostic assays of a viscous material (e.g. sputum) from a cultivation of itc. Mase antibodies can be used for detection and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1124 BP; 299 A; 273 C; 273 G; 279 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                purification of LS-DNase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 6; Fig 3; 32pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       used for the treatment of e.g systemic lupus erythematosus and pulmonary diseases and disorders such as cystic fibrosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated LS-DNase which is resistant to inhibition by actin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-FEB-1996;
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                                                                                                                                                                                                                      GAACCCTTTGTGGTCTGGGTTCCAGTCACCCTACACCGCTGTCAAGGACTTCGTGATTGTC
                                                                                                                                                                                                                                                                                         GTAAAACAAAGCTACCTCTACCACGACTATCAGGCTGGAGACGCAGATGTGTTTTCCAGG 180
                                                                                                                                                                                                                                                                                                                                                                CTTGGAAGAAACACATATAAAGAACAGTATGCCTTTCTCTATAAAGAAAAGCTAGTGTCT 120
                                                                                                                                                                                                                                                                                                                                                                                                       GAGAAGCTGAATGGAAATTCACGAAGAAGCACAACATACAACTATGTGATTAGTTCTCGA 463
                                                                                                                                                                                                                                                                                                                                                                                                                               GAGAAGCTAAACGGAAATTCAAGAAAAGGCATAACATACAACTATGTGATTAGCTCTCGC 60
                               ACAGATGTGAAACGTCGCTGGAATGCAGAGAATTTCATTTTCATGGGTGACTTCAATGCT
                                                                                                                                                         CTTGGAAGAAACACGTACAAAGAGCAGTATGCCTTCGTCTACAAGGAGAAGCTGGTGTCT
GAGCCCTTTGTGGTTTGCATTCCCCCCTTTACTGCTGATCAAGGACTTCGTGATTGTC
                                                                                                                                                                                                                                                                    GTGAAGACAAAATACCACTACCATGACTATCAGGATGGAGACACAGACGTGTTTTCCAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           494;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96US-0597078
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           73.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 435.2; DB 18; Pred. No. 6.9e-128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98; Indels
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RESULT 13
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PFT CDS
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The invention describes a novel isolated human fertility-associated antigen (FAA) and a bovine FAA polypeptide. Human or bovine FAA is useful for increasing the stability of a sperm cell acrosome and for increasing the fertility of a sperm cell acrosome and for increasing the fertility of a human male by administering FAA. Detecting single nucleotide polymorphisms (SNPs) of the human or bovine FAA gene is useful for assaying fertility by detecting the presence or absence with the fertility of the mammal and correlating the presence or absence with the fertility of the mammal. The FAA SNPs are chosen from FAA SNPs 1-34 given in the specification. FAA SNPs are chosen from FAA SNPs 1-34 given in the specification. FAA SNP is also useful for determining the reproductive fitness of a human or bovine, by determining the nucleotide sequence of the FAA SNP, quantifying the fertility of more than one mammal containing the FAA SNP and correlating the frequency of the FAA SNP to the fitness of the mammals. FAA improves the integrity of sperm membranes and increases the capacitation of sperm derived from either fertile or infertile humans. Early genetic identification of infertility
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Fig 2A-E; 54pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel human or bovine fertility-associated antigen useful for stabilising sperm cell acrosome and increasing fertility of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P-PSDB; AAU11518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zhang HM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-APR-2000; 2000US-195225P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fertility-associated antigen; FAA; antiinfertility; sperm cell acrosome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  partial cDNA encoding human fertility-associated antigen (FAA), HC2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-MAR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (ZHAN/) ZHANG H M.
(AXRL/) AX R L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       reproductive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       481
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ax RL;
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/product= "Human FAA"
/note= "Human fertility-associated antigen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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WPI; 2002-066307/09

P-PSDB; AAU11519

Ax RL;

HW,

Zhang

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                                                       fertility-associated antigen (FAA), HC2, one of 4 partial prostate cDNA clones of the novel FAA gene described in the method of the invention.
             facilitates early intervention to determine whether the individual may benefit from fertility treatments to avoid costly and/or emotional problems with attempted inseminations. This sequence encodes the human
                                                                                                                                                                                                                                                                                                                                                                                 240
                                                                                                                                                                                   236
                                                                                                                                                                                                                                                              356
                                                                                                                                                                                                                                                                                                                                                       416
                                                                                                                                                                                                                                                                                                                                                                                                            476
                                                                                                                                                        Gaps
                                                                                                                                                                                                              09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    partial cDNA encoding human fertility-associated antigen (FAA), HC3
improves the prognosis for subsequent attempts at fertilisation and
                                                                                                                                                                                                                                                                                                                 CTACACAGATGTGAAACGTCGCTGGAATGCAGAGAATTTCATTTTCATGGGTGACTTCAA
                                                                                                                                                                                                                                                                                                                                                                                                                               CAAGTTCGTTTGGCTGATCGGGGACCAAGAGGACACCACGGTCAAGAAGAGAGCACAAACTG
                                                                                                                                                                                  CAGGGAACCCTTTGTGGTCTGGTTCCAGTCACCCTACACCGCTGTCAAGGACTTCGTGAT
                                                                                                                                                                                                                                                                                               CTACACAGATGTGAAACGTCGCTGGAATGCAGAGAATTTCATTTCATGGGTGACTTCAA
                                                                                                                                                                                                                                                                                                                                                       TGCTGCTGCTGCTACGTCCCCAAGAAGCCTGGAAGGACATCCGCCTGAGGACGC
                                                                                                                                                                                                                                                                                                                                                                                                             CAAGTTCGTTTGGCTGATCGGGGACCAAGAGGACACCACGGTCAAGAAGAGCACAAAACTG
                                                                                                                                                                                                              1 cagggaaccerrreregreegreegreagecerrecegerereageactregreat
                                                                                                                                                                                                                                         /note= "Human fertility associated antigen, HC3"
'partial
'note= "No start or stop codon given"
/transl_except= (pos:251..253, aa: Arg)
                                                                                                                                                      .
0
                                                                                                                         Score 348.4; DB 24; Length 350;
Pred. No. 1.6e-100;
0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CGCCTATGACAGGATCGTGCTTAGAGGACAAAATATTGTCAACTCTGTTG 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CGCCTATGACAGGATCGTGCTTAGAGGACAAAATATTGTCAACTCTGGTG 526
                                                                                                 88 A; 91 C; 93 G; 78 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           product= "Human FAA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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                                                                                                                            58.9%;
99.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAS17903 standard; cDNA; 350
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                                                                                                                            Query Match
Best Local Similarity 99.7
Matches 349; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (ZHAN/) ZHANG H M.
(AXRL/) AX R L.
                                                                                                 Sequence 350 BP;
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antigen (FAA) and a bovine FAA polypeptide. Human or bovine FAA is useful for increasing the stability of a sperm cell acrosome and for increasing the stability of a perministering FAA. Detecting single conclude polymorphisms (SNPs) of the human or bovine FAA gene is useful for assaying fertility by detecting the presence or absence of a FAA SNP in the mammal and correlating the presence or absence of a FAA SNP in the mammal and correlating the presence or absence of a FAA SNP in the mammal and correlating the presence or absence of a FAA SNP correlating the presence or absence of a FAA SNP in the FAA SNP is also useful for determining the reproductive fitness of a human or bovine, by determining the nucleotide sequence of the FAA SNP quantifying the fertility of more than one mammal containing the FAA SNP and correlating the frequency of the FAA SNP to the correlating the frequency of the FAA SNP to the reproductive fitness of the mammals. FAA improves the integrity of sperm derived from either correlating the capacitation of sperm derived from either correlating the reproductive fitness of the mammals. FAA improves the indevidual may correlating the respective determine whether the individual may correlating for subsequent attempts at fertilisation and the facility recataments to avoid costly and/or emotional correlating estility associated antigen (FAA), HC3, one of 4 partial prostate cDNA concept the novel FAA gene described in the method of the invention.
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                                                                                                                                                                                                                                             The invention describes a novel isolated human fertility-associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Partial cDNA encoding human fertility-associated antigen (FAA), HC4
                                                                                                                               Novel human or bovine fertility-associated antigen useful for stabilising sperm cell acrosome and increasing fertility of a male
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 CTACACGGACGTGAAACACCGCTGGAAGGCGGAGAATTTCATTTTCATGGGTGACTTCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTACACAGATGTGAAACGTCGCTGGAATGCAGAATTTTCATTTTCATGGGTGACTTCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           417 CAAGTTCGTTTGGCTGATCGGGGACCAAGAGGACACCACGGTCAAGAAGAGCACAAAACTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 TATCCCCCTGCACCACCCCCAGAGACATCCGTTAAGGAGATCGATGAGTTGAGGT
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Pred. No. 7.9e-90;
0; Mismatches 22; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 350 BP; 89 A; 93 C; 94 G; 74 T; 0 other;
                                                                                                                                                                                                   Claim 1; Fig 2A-E; 54pp; English
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Fertility-associated antigen; FAA; antiinfertility; sperm cell acrosome; reproductive fitness; single nucleotide polymorphism; SNP; human;

Homo sapiens.

Location/Qualifiers

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The invention describes a novel isolated human fertility-associated cantigen (FAA) and a bovine FAA polypeptide. Human or bovine FAA is useful CC for increasing the stability of a sperm cell acrosome and for increasing the fertility of a human male by administering FAA. Detecting single CC funcleotide polymorphisms (SNPs) of the human or bovine FAA gene is useful for assaying fertility by detecting the presence or absence of a FAA SNP in the mammal and correlating the presence or absence with the fertility CC of the mammal. The FAA SNPs are chosen from FAA SNPs 1-34 given in the Specification. FAA SNP is also useful for determining the reproductive CC fitness of a human or bovine, by determining the nucleotide sequence of the FAA SNP, quantifying the fertility of more than one mammal containing the FAA SNP and correlating the frequency of the FAA SNP to the frequency of the FAA SNP to the CC reproductive fitness of the mammals. FAA improves the integrity of sperm CC membranes and increases the capacitation of sperm derived from either CC fertile bumans. Early genetic identification of infertility CC improves the prognosis for subsequent attempts at fertilisation and CC facilitates early intervention to determine whether the individual may CC consess with attempted inneminations. This sequence encodes the human CC fertility-associated antigen (FAA), HC4, one of 4 partial prostate CDNA CC clones of the novel FAA gene described in the method of the invention.
                                                                                                                                                                                                                                                                   Matches 318;
                                                                                                                                                                                                                                                                                                     Best Local Similarity
                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel human or bovine fertility-associated antigen useful for stabilising sperm cell acrosome and increasing fertility of a
                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 349 BP; 89 A; 91 C; 93 G; 76 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Fig 2A-E; 54pp; English.
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(AXRL/) AX R L.
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GGAACCCTTTGTGGTCTGGTTCCAGTCACCCCTACACCGCTGTCAAGGACTTCGTGATTGT 239
                                                                                                                  GGGAGCCCTTGTGGTCTGGTTCCAATCTCCCCACACTGCTGTCAAAGACTTCGTGATTAT
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/transl_except= (pos: 11..12, aa:Phe)
/note= "This codon has an apparent 1 nucleotide
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                                                                                                                                                                                                                                                           50.8%; Score 300.6; DB 24; 91.6%; Pred. No. 2.6e-85; cive 0; Mismatches 29;
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                                                                        GTTCGTTTGGCTGATCGGGGACCAAGAAGGACACCACGGTCAAGAAGAGCACAAACTGCGC 479
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                                                                                                                                                                                  CACAGATGTGAAACGTCGCTGGAATGCAGAGAATTTCATTTTCATGGGTGACTTCAATGC 359
CTATGACAGGATCGTGCTTAGAGGACAAAATATTGTCAACTCTGTTG
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                                                                                                           CGGCTGCAGCTACGTCCCCAAGAAGGCCTGGAAGAACATCCGCTTGAGGACTGACCCCAG
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Database :
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Listing first 45 summaries
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Perfect score:
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    16154066 seqs, 8097743376 residues
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Gapop 10.0 , Gapext 1.0
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592
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Copyright (c) 1993 - 2002 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length DB	Length	BB	ID	Description
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N	476.8	80.5	896	9	AL546432	AL546432 AL546432
c 3	471.8	79.7	833	9	AL572037	AL572037 AL572037
C 4	469	79.2	931.	9	AL571894	AL571894 AL571894
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7162 xn06e10	064211 H3016H0	989198 og95d05	zj32d04.	qh67e04.	qj82a	34 IL2	ž	53 H30	86387 UI-E-E	3965		0300	5 ui58a02	<u>~</u>	30 xn296)8 60203004	35 7074e	66 60202811	3 60258	0 ws04	Þ	ü	õ	ŏ	8	S	710632	3 we67c07.	38 60308	1 wo91g09.	54 EST34686	39 C0132C0	50 6032)2 C0174C0	36 60255862	G867772	43356 C0168H0	23

ALIGNMENTS

	FEATURES Source	REFERENCE AUTHORS TITLE JOURNAL COMMENT	ACCESSION VERSION KEYWORDS SOURCE ORGANISM	RESULT 1 AL546857 LOCUS DEFINITION
/organism="Homo sapiens" /db xref="taxon:9606" /clone="CSODIO26YK08" /clone_lib="LTI NFL006 PL2" /tissue_type="placenta" /note="Vector: pCMV5PORT 6; Site_1: NotI; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end	Delioscope - centre wattonat de sequencage BP 191 91006 EVRY cedex - France Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr. Location/Qualifiers 1890	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 890) 1 i, W.B., Gruber, C., Jessee, J. and Polayes, D. 1 Li, W.B., Gruber, C., Jessee, J. and normalization Unpublished (2001) Contact: Genoscope Contact: Genoscope	Dilme, mana sequence: AL546857 AL546857.1 GI:12880381 EST. human. Homo sapiens	AL546857 AL546857 LTI_NFL006_PL2 Homo sapiens cDNA clone CSODI026YK08 5

: www.genoscope.cns.fr.

Sequencage

Genoscope - Centre National de Seque BP 191 91006 EVRY cedex - France Email: segreføgenoscope.cns.fr, Web

Location/Qualifiers

FEATURES

Centre National de

/organism="Homo sapiens"

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/clone="Tx Try NPLO06 PL2"
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/closue type="Placenta"
/note="Vector: pcMvSPORT 6; Site_1: NotI; 1st strand cDNA
was primed with a NotI-oligo(df) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pcMvSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact: Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, maryland 20850, USA Fax: (1) 301 610 8371
Email: fliang@lifetech.com URL:
http://fullength.invitrogen.com"
ttp://fullength.invitrogen.com"
1 others

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Gaps 9

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Indels

Score 476.8; DB 9; Pred. No. 3.1e-128; 0; Mismatches 72;

tch 80.5%; al Similarity 87.8%; 520; Conservative (

Query Match

Best Local Matches 5

249

BASE COUNT ORIGIN

Length 896;

266 GAGAAGCTGAACAGAAATTCAAGGAGAGGCATAACGTACAACTATGTGATTAGCTCTCGG 325

1 GAGAAGCTAAACGGAAATTCAAGAAAAGGCATAACATACAACTATGTGATTAGCTCTCGC

CTTGGAAGAAACACATATAAAGAACAGTATGCCTTTCTCTATAAAGAAAAGCTAGTGTCT

61

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386 GTGAAGAGGAGTTATCACTACCATGACTATCAGGATGGAGACGCAGATGTGTTTTCCAGG

GTAAAACAAAGCTACCTCTACCACGACTATCAGGCTGGAGGCGCAGATGTGTTTTCCAGG

446 GAGCCTTTGTGGGTCTGGTTCCAATCTCCCCACACTGCTGTCAAAGACTTCGTGATTATC

GAACCCTTTGTGGTCTGGTTCCAGTCACCCTACACCGCTGTCAAGGACTTCGTGATTGTC

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445 240 505 300 565 360 625

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enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Bco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : http://fulliang@lifetech.com URL : http://fulliangflifetech.com URL : http://fulliangflifetech.com URL : http://fulliangflifetech.com URL : http://fulliangflifetech.com URL : 1 others
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Pred. No. 1.1e-128;
0; Mismatches 71;
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                        RESULT 3
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                                               Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 896)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Pull-length cDNA libraries and normalization

Unpublished (2001)

Contact: Genoscope
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TTCGTTTGGCTGATCGGGGACCAAGAGGACACCCACGGTCAAGAAGAGACCACAAACTGCGCC

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746 TATGACAGGATTGTGCTTAGAGGACAAGAAATCGTCAGTTCTGTTGTTCCCAAGTCAAAC

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bp mRNA linear EST 16-FEB-2001 sapiens cDNA clone CS0DI030YD20 5

AL546432 896 AL546432 LTI_NFL006_PL2 Homo prime, mRNA sequence.

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human.

VERSION KEYWORDS SOURCE ORGANISM

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TTCGTTTGGCTGATCGGGGACCAAGAGGGACACCACGGTCAAGAAGAGCACAAACTGCGCC
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                                                  TTTGTTTGGCTGATCGGGGACCAAGAGGACACCACGGTGAAGAAGAGCACCAACTGTGCA
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Genoscope - Centre National de Sequencage
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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ail: segref@genoscope.cns.fr, V
Location/Qualifiers
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/db_xrefs"taxon:9606"
/clone="CSODIO26YK08"
/clone_lib="LTI NFL006_PL2"
/tissue_type="placenta"
/note="Vector: pCMVSPORT_6; S
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ACAGATGTGAAACGTCGCTGGAATGCAGAGAATTTCATTTTCATGTGGTGACTTCAATGCT
                                                          GAACCCTTTGTGGTCTGGTTCCAGTCACCCCTACACCCGCTGTCAAGGACTTCGTGATTGTC
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                                         GAGCCCTTTGTGGTCTGGTTCCAATCTCCCCACACTGCTGTCAAAGACTTCGTGATTATC
                                                                                                                                                GTGAAGAGGAGTTATNACTACCATGACTATCAGGATGGAGACGCAGATGTGTTTTCCAGG
                                                                                                                                                                         GTAAAACAAAGCTACCTCTACCACGACTATCAGGCTGGAGACGCAGATGTGTTTTCCAGG
                                                                                                                                                                                                    CTTGGAAGAACACATATAAAGAACAATATGCCTTTCTCTACAAGGAAAGGCTGGTGTCT
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AL571894 LTI_NFL006_PL2
~~ime. mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genoscope - Centre National de So
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, 1
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Mammalia, Eutheria,
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AL571894
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Pred. No. 6e-126;
1; Mismatches 7
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449 207

87

267

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/organism="Homo sapiens"

/db_xref="teaxon:9606"

/db_cref="teaxon:9606"

/clone=Inb="NGI CGAP Brn52"

/tissue_type="tumor, 5 pooled (see description)"

/lab host="HAID8"

/note="Organ: brain; Vector: pCMV-SPORT6; Site 1: Sall;

Site 2: Not1; This library represents the normalized version of NCI CGAP Brn35. Cloned unidirectionally.

Primer: Oligo dT. Average insert size 1.19 kb. Tumor types include: mentingioma, oligodendroglioma, astrocytoma (grade II), medulloblastoma, astrocytoma (grade IV).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                666 bp mRNA linear EST 20-OCT-2000 t246h09.yl NCI_CGAP_Brn52 Homo sapiens cDNA clone IMAGE:2291681 5' similar to SW:DHP2 HUMAN Q13609 DNASE I HOMOLOGOUS PROTEIN DHP2 BECURSOR ;, mRNA Sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL, send email to:
info@image.llnl.gov
Insert Length: 1048 Std Error: 0.00
Seq primer: -40RP from Gibco
High quality sequence stop: 431.
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1 (bases 1 to 666)
NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAP), Tumor Gene Index Unpublished (1998)
Contact: Robert Strausberg, Ph.D.
CTACACCGCTGTCAAGGACTTNGTGATTGTCCCCCTGCACACCACCCCTGAGACATCCGT 387
                                                                                                                                                                                                                                                                                                                                              CACCACGGTCAAGAAGAGCACAAACTGCGCCTATGACAGGATCGTGCTTAGAGGACAAAA
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                                                                            386 TAGAGAGATTGATGAGCTGGCTGATGTCTACACAGATGTGAAACGTCGCTGGAATGCAGA
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Detartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bos.
1 (bases 1 to 506)
Takasuga,A., Hirotsune,S., Itoh,R., Jitohzono,A., Suzuki,H., Aso,H. and Sugimoto,Y.
Establishment of a high throughput EST sequencing system using poly(A) tail-removed cDNA libraries and determination of 36,000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AV607154
AV607154 Bos taurus kidney fetus Bos taurus cDNA clone EIKI039B05
AV607154 Bos taurus kidney fetus Bos taurus cDNA clone EIKI039B05
AV607154
AV607154.1 GI:9737527
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    426 ACGGACGTGAAACACCGCTGGAAGGCGGAGAATTTCATTTTCATGGGTGACTTCAATGCC 367
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Shirakawa Institute of Animal Genetics
Odakura, Nashigo, Nishi-shirakawa, Fukushima 961-8061, Japan
TT: 81-248-25-5725
Fax: 81-248-25-5725
                                                                                                                                                                      Email: kazusugi@cocoa.ocn.ne.jp
Single pass sequencing.
This clone was obtained from a polyA-deleted cDNA library.
Location/Qualifiers
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/tissue_type="kidney"
/dev_stage="fetus"
/lab_nost="DH108"
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Pred. No. 3.1e-117,
0; Mismatches 3,
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21570554
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/db_xref="taxon:9913"
/clone="E1KI039B05"
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Best Local Similarity 87.5%;
Matches 471; Conservative
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                           cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLN
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
http://image.lln.gov
http://image.lln.gov
http://image.lln.gov
http://image.lln.gov
http://image.lln.gov
http://image.lln.gov
                                                                                                                                                                                                                                                                                                                                             B1522352
603081420T1 NIH_MGC_120
mRNA sequence.
B1522352
                                                                                                                                       Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies,
                                                                                                                                                                                     1 (bases 1 to 695)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Unpublished (1999)
                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae
                                                                                                                                                                                                                                                                                   Homo sapiens
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quality sequence start: 18 quality sequence stop: 695
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Pred. No. 3.4e-115;
0; Mismatches 67;
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Homo
                                                                                                                                                                                                                                                                                                                                                                          bp mRNA linea
sapiens cDNA clone
                                                                                                                                         Inc.
                                                                                                                                                                                                     Gene
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IMAGE:5220532 3',
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VERSION KEYWORDS

SOURCE

house mouse

ACCESSION

AW543356 C0168H07-3 NIA Mouse E musculus cDNA clone C0 AW543356 AW543356.1 GI:7185773

642 bp mRNA linear EST 31-AUC e E7.5 Extraembryonic Portion cDNA Library C0168H07 3', mRNA sequence.

31-AUG-2000

GI:7185773

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RESULT 8
AW543356/c
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Best Local S
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                                                                                                                  AAGCTTACAGGTTGTCTGAATCGAAGGCC
                                                                                                                                                                                                                                  CCAAGAGGACACCACGGTCAAGAAGAGCACAAACTGCGCCTATGACAGGATCGTGCTTAG
                                                                                                                                                                                                                                                                                                  GAAGGCCTGGAAGGACATCCGCCTGAGGACGGACCCCAAGTTCGTTTTGGCTGATCGGGGA
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                                                                                            AAGCTTACAAGCTGACTGAAGAGGAGGCC
                                                                                                                                                       AGGACAAGAATCGTCAGTTCTGTTGCTCCCAAGTCAGAACAGTGTTTTTGACTTCCAGA
                                                                                                                                                                                    AGGACAAAATATTGTCAACTCTGGTGGTCCTCAATCA-AACCTCGTCTTTGATTTCCAGA 559
                                                                                                                                                                                                                                                                                GAAGGCGGAGAATTTCATTTCATGGGTGACTTCAATGCCGGCTGCAGCTACGTCCCCAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         496;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 n 71.1%;
Similarity 87.2%;
96; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Organ: pooled pancreas and spleen; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: ECORV (destroyed); RNA source anonymous pool of spleen and pancreas from 28 yo male. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.5 kb, insert size range 1-2.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 025. Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="IMAGE:5220532"
/clone_lib="NIH_MGC_120"
/lab_host="DH10B"
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Pred. No. 5.7e-112;
0; Mismatches 70;
                                                                                            127
                                                                                                                         885
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450

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/db_xref="taxon:10090"
/clone="INAGE:4912893"
/clone="INAGE:4912893"
/clone="INAGE:4912893"
/clone="CGAP_262"
/lab host="DH10B (TI phage-resistant)"
/note="Organ: salivary gland; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1:3 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BG867772 825 bp mRNA linear EST 29-MAY-2001
602786883F1 NCI_CGAP_SG2 Mus musculus cDNA clone IMAGE:4912893 5',
mRNA sequence.
BG867772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
clone distribution: MGC clone distribution information can be found through the I.W.A.G.E. Consortium/LLNL at:
http://mage.llhl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosto
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
1 (Bases 1 to 825)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            162 ATAGTCAACTCCGTGGTCCCCGTTCCAGTGGCGTCTTTGACTTTCAGAAAGCTTATGAC 103
                                                                                                                           CAGAACATTCGTTTGAGGACGGACCCCAAGTTTGTTTGGCTGATTGGGGACCAAGAGGAC 223
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Rodentia; Sciurognathi; Muridae; Murinae;
AGAGAGATTGATGAGCTGGCTGATGTCTACACAGATGTGAAACGTCGCTGGAATGCAGAG 330
                                                                                                                                                                                                                                                    AATTTCATTTTCATGGGTGACTTCAATGCTGGCTGCAGCTACGTCCCCAAGAAGGCCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACCACGGTCAAGAAGAGCACAAACTGCGCCTATGACAGGATCGTGCTTAGAGGACAAAAT
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                                                                                                                                                                                                                                                                                                                               391 AAGGACATCCGCCTGAGGACGGACCCCAAGTTCGTTTGGCTGATCGGGGACCAAGAGGAC
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82.7%; Pred. No. 1.5e-107;
iive 0; Mismatches 100;
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/strain="FVB/N"
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Best Local Similarity 82.7
Matches 488; Conservative
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TITLE
JOURNAL
COMMENT
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/dev_stage="7.5dpc Embryo"
/lab_host="DH10B"
/note="Vector: pSPORT1 (Gibco/BRL Life Technology);
/note="Vector: pSPORT1 (Total RNAs were extracted from 5 EPC. The double-stranded cDNA was synthesized by Gibco's kit with an Oligo(dT) primer [NotI primer-adapter
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                                                                                                                               Wang, X., Grahovac
Doi, H., Wood, W.H.
               Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Musinae; Musina
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/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="niaEST:C0168H07-3"
/db_xref="taxen:10090"
/clone="C0168H07"
/clone="C10168H07"
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                                                                                                                                                                                                                                                                                                                            Contact: George J. Kargul
Laboratory of Genetics
National Institutes of Health
National Institute on Aging/National Institutes of Health
Sassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@1gsun.grc.nia.nih.gov
Plate: C0168 row: H column: 07
Seq primer: -21M13 Forward
High quality sequence stop: 642
POLYA=Yes
                                                                                                                        Tanaka, T.S., Jaradat, S.A., Lim, M.K., Kargul, G.J., Wang, X., M.J., Pantano, S., Sano, Y., Piao, Y., Nagaraja, R., Doi, H., W III, Becker, K.G. and Ko, M.S.H.
Genome-wide expression profiling of mid-gestation placenta embryo using a 15,000 mouse developmental cDNA microarray Proc. Natl. Acad. Sci. U.S.A. 97 (16), 9127-9132 (2000) 20381348
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                                                                                  CDNA Library Preparation: CLONETECH Laboratories, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
                                                                                                                                                                                                               NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
                                                                                                                                                                                                                                                          Bukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 825)
                                                                                                                                                                                                                                                                                                                                                                            Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.
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organism="Homo sapiens"
/db_xref="taxon:9606"
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RESULT 11 AW543802/c LOCUS

DEFINITION

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620 bp mRNA linear EST 31-AUG-20 C0174C07-3 NIA Mouse E7.5 Extraembryonic Portion cDNA Library Mus musculus cDNA clone C0174C07 3', mRNA sequence.

VERSION KEYWORDS

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SOURCE

house mouse

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APACAGGGTCTTGACTTCCAGAAAGCTTCCAGGCTGACTGTAGAAGAGGCCTTG
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                                                                                                                 CATATGACAGGATTGGTGCTTAGCAGGCACAAGAAATCGTCCAGTCTGTCGTCCCAAGTC
                                                                                                                                                        CCTATGACAGGA-TCGTGCTTAGAGGACAAAATATTGTCAACTCTGGTGGTCCTCAATCA 537
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                                                                                                                                                                                                                                                                                                                                             CGGCTGCAGCTTACGTCCCAAGAAGGTCTGGAACGAACATCCGCTTGAGGACTGACCCCA
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/clone=lib="NIH_MGC_61"
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/lab_host="pH10B (T1 phage-resistant)"
/note="Organ: testis; Vector: pDNR-LIB (Clontech); Site_1:
/note="Organ: pDNR-LI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Library."
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82.5%;
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Pred. No. 9.5e-105;
0; Mismatches 101;
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/organism="Homo sapiens"
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Best Local Similarity
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/dev stage="7.5dpc Embryo"
/dev stage="7.5dpc Embryo"
/lab-host="DH10B"
/note="Vectors: DSPORTI (Gibco/BRL Life Technology);
Site 1: Sall; Site 2: NotI; Total RNAs were extracted from Site 1: Sall; Site 2: NotI; Total RNAs were extracted from Site 1: Sall; Site 2: NotI; Total RNAs were extracted from Gibco's kit with an Oligo (GT) primer (NotI primer-adapter from GibcoBRL)
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                                                                                                                                    Tanaka, T.S., Jaradat, S.A., Lim, M.K., Kargul, G.J., Wang, X., Grahovac, M.J., Pantano, S., Sano, Y., Piao, Y., Nagaraja, R., Doi, H., Wood, W.H.
III, Becker, K.G. and Ko, M.S.H.
Genome-wide expression profiling of mid-gestation placenta and embryo using a 15,000 mouse developmental cDNA microarray proc. Natl. Acad. Sci. U.S.A. 97 (16), 9127-9132 (2000)
                   Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="NIA Mouse E7.5 Extraembryonic Portion cDNA_Library"
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                                                                                                                                                                                                                                                                                                                                                   Contact: George J. Kargul
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
National Institute on Aging/National Institutes of Health
Sassall Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@1gsun.grc.nia.nih.gov
Plate: C0174 row: C column: 07
Seq primer: -21M13 Forward
High quality sequence stop: 620
POLYA=Yes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="niaEST_C0174C07-3"
/db_xref="taxon:10090"
/clone="C0174C07"
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/strain="C57BL/6J"
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COMMENT
                                                                                                                                                    AUTHORS
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/ db xref="taxon:9606" |
/ db xref="taxon:9606" |
/ clone="IMAGE:527217" |
/ clone="IMAGE:527217" |
/ clone="IMAGE:527217" |
/ lab host=="DH10B" |
/ lab host=="DH10B" |
/ lab host=="DH10B" |
/ loce="Organ: testis; Vector: pBluescriptR (modified pBluescript KS+); Site=]: BamH1; Site=2: SalI-Xh0I (gtcgag pBluescript KS+); Site=1: BamH1; Site=2: SalI-Xh0I (gtcgag pSize-selected for average insert size 2: 2kb and normalized to R0T 5. This is a primary library enriched for full-length clones and constructed using the caperation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library."
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Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue brocurement: Miklos Palkovits, M.D., Ph.D.

CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki

Toshiyuki and Piero Carninci (RIKEN)

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LIML at:

thtp://image.llnl.gov

Plate: LLAM11688 row: n column: 22

High quality sequence stop: 628.
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                          260 ACCCCAAGTTTGTTTTGGCTGATTGGGGACCAAGAGGACACTACGGTCAAGAAGAGTACCA 201
                                             120 TCAACGCCGGCTGTAGCTATGTCCCCAAGAAGGCCTGGCAGAACATTCGTTTGAGGACGG 261
                                                                                                                                                                                                                                                                                                                                                                                                                                      473 ACTGCGCCTATGACAGGATCGTGCTTAGAGGACAAAATATTGTCAACTCTGGTGGTCCTC
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 9.4e-103;
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SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS
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                                                                                                                                                                                                                                                                                 Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleos
Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae
1 (bases 1 to 610)
Tanaka, T.S., Jaradat, S.A., Lim, M.K., Kargul, G.J., Wang, X., (
,M.J., Pantano, S., Sano, Y., Piao, Y., Nagaraja, R., Doi, H., Wood, M.S., H.
III, Becker, K.G. and Ko, M.S. H.
Genome-wide expression profiling of mid-gestation placenta; embryo using a 15,000 mouse developmental cDNA microarray
Proc. Natl. Acad. Sci. U.S.A. 97 (16), 9127-9132 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         417;
                                                                                                                                                                Contact: George J. Kargul
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, t
Email: cdna@lgsun.grc.nia.nih.gov
Plate: C0132 row: C column: 04
Seq primer: -21M13 Forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AW540389 610 bp mRNA linear EST 31-AUG-200 C0132C04-3 NIA Mouse E7.5 Extraembryonic Portion cDNA Library Mus musculus cDNA clone C0132C04 3', mRNA sequence.
                                                                                                                                    High quality sequence stop: 610 POLYA=Yes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AW540389.1
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             /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="niaEST:C0132C04-3"
/db_xref="taxon:10000"
/clone="C0132C04"
                                                                                                                   ocation/Qualifiers
   clone
_lib="NIA Mouse E7.5 Extraembryonic
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                                                                                                                                                                                                                                                                                                                                                                                                                    Muridae; Murinae;
 Portion
                                                                                                                                                                                                                                                                                                                                                                                                                                      Euteleostomi;
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Wood, W.H.
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RESULT 14
AW915564
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Best Local Similarity
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                                                                                                                   543
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                                                                                                                                                                                                                                                                                                                                                                                                                       AGATGTGAAACGTCGCTGGAATGCAGAGAATTTCATTTTCATGGGTGACTTCAATGCTGG
                                                                                                                                                                                                                                                                          CGTTTGGCTGATCGGGGACCAAGAGGACACCACGGTCAAGAAGAGCACAAACTGCGCCTA 482
                                                                                                                                                                                                                                                                                                                                          CTGCAGCTACGTCCCCAAGAAGGCCTGGAAGGACATCCGCCTGAGGACGACCCCCAAGTT
                                                                              CGTCTTTGACTTTCAGAAAGCTTATGACTTGTCTGAGGAGGAGGCCCTGG
                                                                                                           CGTCTTTGATTTCCAGAAAGCTTACAGGTTGTCTGAATCGAAGGCCCTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGGAAGAAACACGTACAAAGAGCAGTATGCCTTCGTCTACAAGGAGAAGCTGGTGTCTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGGAAGAAACACATATAAAAGAACAGTATGCCTTTCTCTATAAAGAAAAGCTAGTGTCTGT 122
                                                                                                                                                      TGACAGGATTGTGCTTTGTGGACAAGAGATAGTCAACTCCGTGGTTCCCCGTTCCAGTGG
                                                                                                                                                                                            GGATGTGAGAAGCCAGTGGAAGACAGAGAATTTCATCTTCATGGGTGATTTCAACGCCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTTGCACACACTCCCGAGACCTCCGTTAAAGAGATAGATGAGCTGGTCGATGTCTACAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             by long-range high fidelity PCR using Takara's Ex Taq polymerase. Then, the cDNAs were purified by phenol/chloroform and by Centricon 100. The cDNAs were digested with Sall and NotI enzymes. Then, the cDNAs were size selected by Gibco's Size Fractionation Column. The cDNAs were cDNAs were cloned into Sall/NotI site of pSPORT1 plasmid vector. The DH10B E. coli host was transformed with the lighting mixture by chemical method. The library was constructed by Xiaohong Wang."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         from 0.8ug of mRNA. The double-stranded cDNAs were treated with T4 DNA polymerase and purified by ethanol-precipitation. The cDNAs were ligated to Lone-linker Li-Sal3 (include Sal1 sequence). The cDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gibco's kit with an Oligo(dT) primer [NotI primer-adapter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Vector: psport1 (Gibco/BRL Life Technology);
Site_1: Sall; Site_2: Not1; Total RNAs were extracted from
5 EPC. The double-stranded cDNA was synthesized by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    were purified by phenol/chloroform and separated from free linkers by Centricon 100. Then, cDNAs were amplified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /sex="unknown"
/dev_stage="7.5dpc Embryo"
/lab_host="DH10B"
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83.0%;
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Pred. No. 9.1e-102;
0; Mismatches 90;
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LOCUS DEFINITION

AW915564 EST346868 Normalized RGICW80 5' end, mRNA

sequence 668 bp rat embryo,

> Bento mRNA

Soares

linear I res Rattus

EST 25-MAY-2000 s sp. cDNA clone

sp.

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188 c
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Best Local S:
Matches 422
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ORIGIN
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                      RESULT 15
AI927844/c
                                                LOCUS
DEFINITION
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                                                                                                     ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                             ORGANISM
                                                                                                                                                                                                                     AUTHORS
TITLE
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                                                                  Euteleostomi;
Murinae;
                                                                                                                                                    (REST) Catalog & Rat
                                                                                                                                                                                                                                                                                                                                 /organism="Rattus sp."
/organism="Rattus sp."
/db.xref="taxon:10118"
/clone="RGICW80"
/clone="RGICW80"
/clone="Normalized rat embryo, Bento Soares"
/dev_stage="embryo 8, 12, 18 dpc"
/note="vector: pT7T3Pac; Site_1: EcoRI; Site_2: NotI"
/note="vector: pT7T3Pac; Site_1: EcoRI; Site_2: NotI"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   80 AAGAACAGTATGCCTTTCTCTATAAAGAAAAGCTAGTGTCTGTAAAACAAAGCTACCTCT 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         140 ACCACGACTATCAGGCTGGAGACGCAGATGTGTTTTCCAGGGAACCCTTTGTGGTCTGGT 199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59
                                                                                                           (bases 1 to 668)
Lee, N.H., Glodek, A., Chandra, I., Mason, T.M., Quackenbush, J.,
Kerlavage, A.R. and Adams, M.D.
Kar Genome Project: Generation of a Rat EST (REST) Catalog &
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                                                                  Craniata; Vertebrata; E
Sciurognathi; Muridae;
                                                                                                                                                                                                                        20850, USA
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                                                                                                                                                                             Unpublished (1998)
Contact: Lee, NH
The Institute for Genomic Research
The Institute for Gener Drive, Rockville, MD 201
Tel: (301)-838-3529
Fax: (301)-838-0208
Email: nhlee@evigr.ox
Email: nhlee@evigr.ox
tel#703-365-2700 for further information
Seq primer: M13 Reverse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 383.8; DB 10;
Pred. No. 4.2e-101;
0; Mismatches 72;
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                                                                  Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
             GI:8081263
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                                                                                                                                                                      Gene Index
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Rattus sp.
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                                                                                                  Rattus.
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Email: buck, M.D., Ph.D.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Preparation: M. Sergi Lennon, Ph.D.
DNA Sequencing by: Mashingcon University Genome Sequencing Center
Clone distribution: NCI-CGAP Clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/imag/imag-image.html
Insert Length: 739 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 426.
High quality sequence stop: 426.
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w091g09.x1 NCI CGAP Kid11 Homo sapiens cDNA clone IMAGE:2462752 3' similar to SW:DHP2 HUMAN Q13609 DNASE I HOMOLOGOUS PROTEIN DHP2 PRECUSSOR; , mRNA Sequence.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 784)
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National Cancer Institute, Cancer Genome Anatomy Project
Tumor Gene Index
Unpublished (1997)
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86.7%; Pred. No. 5.1e-101;
cive 0; Mismatches 65;
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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                                             466 AGCACAAACTGCGCCTATGACAGGATCGTGCTTAGAGGACAAAATATTGTCAACTCTGGT 525
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        586 GCCCTGG 592
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Search completed: December 9, 2002, 12:18:03 Job time : 1339.4 secs

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           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.
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                                                                             ; LOCATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PBLENTIN RC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/88/640,765A
FILING DATE: 06-MAY-1996
CLASSIFICATION 04-35
PRIOR APPLICATION NUMBER: JP 6239518
APPLICATION NUMBER: JP 6239518
FILING DATE: 06-SEP-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 27555
REFERENCE/DOCKET NUMBER: 73362
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 616-5700
INFORMATION: FOR SEO ID NO: 2:
       Query Match
Best Local Similarity
Matches 505; Conserv
                                                                                                                                                                                                                                    TELEFAX: (312) 616-570
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                 LENGTH: 1208 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
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ADDRESSEE: Leydig, V
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Tanuma, TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: Two Prud
CITY: Chicago
STATE: Illinois
COUNTRY: USA
                                                                                                                NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 60601
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         Conservative
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                        76.5%;
85.3%;
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US-09-644-600-9
US-09-044-600-1
US-09-644-600-18
US-09-484-970B-63
US-09-484-970B-63
US-09-28-986-21
US-08-162-809-11
US-08-162-809-11
US-08-162-809-11
US-08-162-809-11
US-08-162-809-11
US-09-228-986-21
US-09-238-760-5
US-09-330-770-5
US-09-330-770-5
US-09-330-770-5
US-09-330-770-5
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       Score 452.8; DB 1;
Pred. No. 5.4e-132;
0; Mismatches 87;
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; Sequence 2, Application US/09073613
; Patent No. 6143875
; GENERAL INFORMATION:
; APPLICANT: Tannam, Sei-ichi
; TITLE OF INVENTION: ANTIBODY TO NOVEL DEOXYRIBONUCLEASE
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leydig, Voit & Mayer
; STREET: Two Prudential Plaza, Suite 4900
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Version #1.25
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Vei
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/073,613
FILING DATE: 06-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
FILING DATE:
APPLICATION NUMBER: JP 6239518
FILING DATE: 06-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: LARCHER, CAROL
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APPLICATION NUMBER: 08/640,765
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US-09-073-613-2
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                                                                                                                                                                                                                                                                                                                  Length 1208;
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85.3%; Pred. No. 5.4e-132;
iive 0; Mismatches 87;
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Fatent No. 5279823
GENERAL INFORMATION:
APPLICANT: Frenz, John
APPLICANT: Shire, Steven J.
APPLICANT: Sliwkowski, Mary B.
TITLE OF INVENTION: PURIFIED FORMS OF DNase
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
REGISTRATION NUMBER: 35243
REFRENCE/DOCKET NUMBER: 85515
TELECOMUNICATION INFORMATION:
TELEPHONE: (312) 616-5700
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
LENGTH: 1208 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
TOPOLOGY: linear
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 85.3
Matches 505; Conservative
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12..941
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, LOCATION:
US-09-073-613-2
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US-07-895-300A-2
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARATERISTICS:
LENGTH: 1039 bases
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
77-895-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Sim
Matches 317;
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FILING DATE: 19920608
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Hensley, Max D.
REGISTRATION NUMBER: 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 27,043
REFERENCE/DOCKET NUMBER: 74
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                      ATTGTCAACTCTGGTGGTCCTCAATCAAACCTCGTCTTTGATTTCCAGAAAAGCTTACAGG 570
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                                                                                              ACCACGGTCAAGAAGAGCACAAACTGCGCCTATGACAGGATCGTGCTTAGAGGACAAAAT
                                                                                                                                          TCATCCATCCGCCTGTGGACAAGCCCCACCTTCCAGTGGCTGATCCCCGACAGCGCTGAC
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CTCCGAGGCGCCGTTGTTCCCCGACTCGGCTCTTCCCCTTTAACTTCCAGGCTGCCTATGGC
                                                                    ACCACAG----CTACACCCACGCACTGTGCCTATGACAGGATCGTGGTTGCAGGGATGCTG
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56.7%;
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Pred. No. 4.4e-37;
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-3562
TELEPAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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Patent No. 6440412
                                                                                                                                                                                                                                                                                                                                                            Matches 317; Conservative
                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
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APPLICATION NUMBER: 08/942561

FILING DATE: 01-OCT-1997

ATTORNEY/AGENT INFORMATION:

NAME: Johnston, Sean A.

REGISTRATION NUMBER: 35,910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
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MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winbatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/638,112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Shire, Steven J.
APPLICANT: Sliwkowski, Mary B
TITLE OF INVENTION: PURIFIED
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
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CITY: South San Francisco
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                                                                   TTCACAGAGGTCAGGGAGTTTGCCATTGTTCCCCCTGCATGCGGCCCCCGGGGGACGCAGTA 648
                                                                                                     TACACCGCTGTCAAGGACTTCGTGATTGTCCCCCTGCACACCACCCCTGAGACATCCGTT 270
                                                                                                                                           TTCGTGTACAGGCCTGACCAGGTGTCTGCGGTGGACAGCTACTACGATGATGGCTGC 528
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D FORMS OF DNase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: patin (Genertech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/10519
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Johnston, Sean A. REGIGTRATION NUMBER: 35,910 REFERENCE/DOCKET WUMBER: 79 TELECOMMUNICATION INFORMATION: TELEPHONE: 415/225-3562
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                415/952-9881
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COMPUTER READABLE FORM:
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                             rgcagctacgtccccaagaaggcctgg
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                                                                                                            391 AAGGACATCCGCCTGAGGACGGACCCCAAGTTCGTTTGGCTGATCGGGGACCAAGAGGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application PC/TUS9305136
GENERAL INFORMATION:
APPLICANT: Generatech, Inc.
TITLE OF INVENTION: PURIFIED FORMS OF DNase
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
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STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
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3R: 747PCT
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US9.
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Best Local Similarity 56.7%;
Matches 317; Conservative
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REGISTRATION NUMBER: P35
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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TELEX: 9
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Generated, Inc.
TITLE OF INVENTION: Therapy
NUMBER OF SEQUENCES:
ADDRESSEE: Generated, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
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                                                           271 AGAGAGATTGATGAGCTGGCTGATGTCTACACAGATGTGAAACGTCGCTGGAATGCAGAG
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                                                                                                                  GENERAL INFORMATION:
APPLICANT: Frenz, John
APPLICANT: Shire, Steven J.
APPLICANT: Sliwkowski, Mary B.
TITLE OF INVENTION: PURIFIED FORMS OF
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/08458367 Patent No. 5783433
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Best Local Similarity 56.7
Matches 317; Conservative
                ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 1039 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTGTCAACTCTGGTGGTCCTCAATCAAACCTCGTCTTTGATTTCCAGAAAGCTTACAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTCCGAGGCGCCGTTGTTCCCGACTCGGCTCTTCCCCTTTAACTTCCAGGCTGCCTATGGC
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WinPatin (Genentech)
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56.7%;
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Pred. No. 4.4e-37;
0; Mismatches 236;
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Sest Local Similarity 56.5%;
Matches 316; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEO ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1039 base pairs
TYPE: Nucleic Acid
STRANDENESS: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 30-NO. 57834
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/11
FILING DATE: 02-Sep-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: 415/225-3562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 08-Jun-1992 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 22-Mar-1995 PRIOR APPLICATION DATA:
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APPLICATION NUMBER: 08/409631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Johnston, Sean A. REGISTRATION NUMBER: 35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 08/348284
                                                                                                                                                ACCACGGTCAAGAAGAGCACAAACTGCGCCTATGACAGGATCGTGCTTAGAGGACAAAAT
                                                                                                                                                                                                                                       AAGGACATCCGCCTGAGGACCGGACCCCAAGTTCGTTTGGCTGATCGGGGACCAAGAGGAC
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                                    CTCCGAGGCGCCGTTGTTCCCGACTCGGCTCTTCCCTTTAACTTCCAGGCTGCCTATGGC
                                                                           ATTGTCAACTCTGGTGGTCCTCAATCAAACCTCGTCTTTGATTTCCAGAAAGCTTACAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTCACAGAGGTCAGGGAGTTTGCCATTGTTCCCCTGCATGCGGCCCCCGGGGGACCGAGTA
                                                                                                                      ACCACAG---CTACACCCACGCACTGTGCCTATGACAGGATCGTGGTTGCAGGGATGCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 147.8; DB 1; Pred. No. 1.4e-36;
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                                                                                                                                           1429 Accaccacracr -- Agraccaacracecrraceaceraregraticaregraterae 1485
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                                            1369 TCATCGAÍTCGTCTGCGCÁCCTCGTCGACCÍTCCAGTGGCTGATCCCGGACTCCGCTGAC 1428
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  391 NAGGACATCCGCCTGAGGACGGACCCCAAGTTCGTTTGGCTGATCGGGGACCAAGAGGAC 450
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                                                                                              ACCACGGTCAAGAAGAGCACAAACTGCGCCTATGACAGGATCGTGCTTAGAGGACAAAAT
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GENERAL INFORMATION:
APPLICANT: EPENETOS, AGAMEMNON A.
APPLICANT: SPOONER, ROBERT A.
APPLICANT: DEONARAIN, MAHENDRA
TITLE OF INVENTION: Compounds for targeting
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: MCAULAY NISSEN GOLDBERG KIEL & HAND, LLP
STREET: 261 MADISON AVENUE
CITY: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: DatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/491,988
FILING DATE: 18-DEC-1995
CLASSIFICATION: 42-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 117.2; DB 2;
Pred. No. 6.6e-27;
0; Mismatches 258;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 14, Application US/08491988
Patent No. 5973116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: GOLDBERG, JULES E.
REGISTRATION NUMBER: 24,408
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-986-4090
TELEPHONE: 212-986-4090
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53.0%;
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STRANDEDNESS: single
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MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
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US-08-491-988-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1615;
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                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: MCAULAY INSSEN GOLDBERG KIEL & HAND, LLP
STREET: 261 MADISON AVENUE
CITY: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/491,988
FILING DATE: 18-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6.5e-27;
                                                                                                                                                                                                       APPLICANT: EPENETOS, AGAMEMNON A.
APPLICANT: SPOONER, ROBERT A.
APPLICANT: DEONARAIN, MAHENDRA
TITLE OF INVENTION: Compounds for targeting
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19.8%; Score 117.2;
53.0%; Pred. No. 6.56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                             US-08-491-988-15; Sequence 15, Application US/08491988
; Patent No. 5973116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: GOLDBERG, JULES E.
REGISTRATION NUMBER: 24,408
TELECOMMUNICATION INFORMATION:
TELEFAX: 212-886-4090
TELEFAX: 212-886-4090
TELEFAX: 212-818-9479
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
946 CTGAGTGACCAACTGGCCC 964
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Best Local Similarity 53.0
Matches 298; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 10016-2391
                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
HYPOTHETICAL:
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                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 10016-2391
ZIP: 10016-2391
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Ver
CURRENT APPLICATION DATA:
""DITTATION NUMBER: US/08/491,988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 13, Application US/08491988 Patent No. 5973116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Vatent No. 5973116
GENERAL INFORMATION:
                                                                                                     TELEFAX: 212-818-9479
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1648 base pair
                                                                                                                                                                                    NAME: GOLDBERG, JULES E.
REGISTRATION NUMBER: 24,408
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-986-4090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1495
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CORRESPONDENCE ADDRESS:
ADDRESSEE: MCAULAY NISSEN GOLDBERG KIEL & HAND,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: EPENETOS, AGAMEMNON A.
APPLICANT: SPOONER, ROBERT A.
APPLICANT: DEGNARAIN, MAHENDRA
MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1555 CTTTCGAACGAAATGGCGCTGG 1576
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                                                        LENGTH: 1648 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ITLE OF INVENTION: Compounds for targeting
                                                                                                                                                                                                                                                                                                     FILING DATE: 18 CLASSIFICATION:
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                                        TOPOLOGY:
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                                          linear
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                                                                                                                                                                                                                                                                                                                                                                                          Version
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Best Local Similarity 53.0
Matches 298; Conservative
1579
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                                                                                                                                                                                                                                                                                                                                                                                                                                        1282 GCTGAAATCAACTCTCTGTACGACGTTTACCTGGACGTTCAGCAGAAATGGCACCTGAAC 1341
                                           571
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                                                                                                                                                                                                                                                                                                         391
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                                                                                                                                                                                                                                                                                       AAGGACATCCGCCTGAGGACGGACCCCAAGTTCGTTTGGCTGATCGGGGACCAAGAGGAC 450
CTTTCGAACGAAATGGCGCTGG 1600
                                                                                                                            ATTGTCAACTCTGGTGGTCCTCAATCAAACCTCGTCTTTGATTTCCAGAAAGCTTACAGG 570
                                                                                                                                                                                                                   ACCACGGTCAAGAAGAGCACAAACTGCGCCTATGACAGGATCGTGCTTAGAGGACAAAAAT 510
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTTCTCTATAAAGAAAAGCTAGTGTCTGTAAAACAAAGCTACCTCTACCACGAC---TAT 150
                                        TTGTCTGAATCGAAGGCCCTGG
                                                                                      CTGCAGTCTTCTGTTGTACCGGGTAGCGCGGCCCCGTTCGACTTCCAGGCTGCATATGGT 1578
                                                                                                                                                                                                                                                              TCATCGATTCGTCTGCGCACCTCGTCGACCTTCCAGTGGCTGATCCCGGACTCCGCTGAC 146:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGAGAGATTGATGAGCTGGCTGATGTCTACACAGATGTGAAACGTCGCTGGAATGCAGAG 330
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                                           592
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Pred. No. 6.6e-27;
0; Mismatches 258;
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US-08-468-012A-1
                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/08468012A Patent No. 5830744 GENERAL INFORMATION:
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/46
FILING DATE: 6 JUNE 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94
                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: HUNDMER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                 MEDIUM TYPE: 3.5 INC
                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                     COUNTRY: U
ZIP: 07068
                                                                                                                                                                                                                                                                         STREET:
                                                                                                                                                                                                                                                                                            ADDRESSEE:
                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
                                                                                                                                                                                                                                     ROSELAND
: NEW JERSEY
                                                                                                                                                                                                                                                                         E: CARELLA, BYRNE, BAIN, GILFILLAN
E: CECCHI, STEWART & OLSTEIN
6 BECKER FARM ROAD
                                                                                                                                                                                                                      USA
                                                                                                                                                                                                                                                                                                                                                                                        RUBEN,
                                                                                                                                                                                                                                                                                                                                                                                      ET AL.
                                                                                                                                                                 INCH DISKETTE
                                                                                                                                                                                                                                                                                                                                                                   Human DNase
                                                                           US/08/468,012A
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PCT/US94/04954

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APPLICANT: Lu, Aina
TITLE OF INVENTION: Protein Kinase Homologs
FILE REFERENCE: PF-0614 US
CURRENT APPLICATION NUMBER: US/09/173,581A
CURRENT FILING DATE: 1998-10-15
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PERL Program
SOFTWARE: PERL Program
SOFTWARE: PERL PROGRAM
SEQ ID NO 10
LENGTH: 1427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 \mu Sequence 10, Application US/09173581A \mu Patent No. 6013455
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APPLICANT: Tang, Y. Tom
APPLICANT: Hillman, Jennifer L.
APPLICANT: Wue, Henry
APPLICANT: Guegler, Karl J.
APPLICANT: Gorley, Neil C.
APPLICANT: Aprican, Yalda
APPLICANT: Azimzai, Yalda
APPLICANT: Lu, Aina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 58.6%;
Matches 198; Conservative
                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 1055 BASE PAIRS
TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
                                                                                                                                                                                                                                                                                     201-994-1744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Homo sapiens
FEATURE: -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: LINEAR MOLECULE TYPE: CDNA
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US-09-173-581-10
                                                                                                                                                                                                                                                                                            TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-054-989-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          340 TTCATGGGTGACTTCAATGCTGGCTGCAGCTACGTCCCCAAGAAGGCCTGGAAGGACATC 399
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Pred. No. 2.2e-26;
1; Mismatches 139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             659 cedeccaccaccacracaccrardacceccredrect 696
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, ADDRESSEE: CECCHI, STEWART & OLSTEIN STREET: 6 BECKER FARM ROAD
                                                                                                                                       325800-428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/054,989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   160 GACGCAGATGTGTTTTCCAGGGAACCCTT
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MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/468,012
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Patent No. 6251648
GENERAL INFORMATION:
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TITLE OF INVENTION: Human DNase
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                             ATTORNEY/AGENT INFORMATION:
NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33,073
REFRENCE/DOCKET NUMBER: 3258.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
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SOFTWARE: WORD PERFECT 5.1
                                                                                                                                                                                                                                     INFORMATION FOR SEQ 1D NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 1055 BASE PAIRS TYPE: NUCLEIC ACID STRANDEDNESS: SINGLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19.5%;
FILING DATE: 5 MAY 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 58.6
Matches 198; Conservative
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INDW JERSEY
RY: USA
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STATE: NE
COUNTRY:
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340 TICATGGGTGACTICAATGCTGGCTGCAGTACGTCCCCAAGAAGGCCTGGAAGGACATC 399
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Pred. No. 2.2e-26;
1; Mismatches 139;
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FILING DATE: 6-JUNE-1995
APPLICATION NUMBER: PCT/US94/04954
FILING DATE: 5 MAY 1994
ATTORNEY/AGENT INFORMATION:
NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33,073
REFERENCE/DOCKET NUMBER: 325800-428
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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RESULT 15
US-08-924-440-1
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                                                                                                                                                                                                                                                                                                                                                                                 US-09-420-915-10
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NUMBER OF SEQ ID NOS: 18
SOFTWARE: PERL Program
SEQ ID NO 10
LENGTH: 1427
Sequence 1, Application US/08924440 Patent No. 5871550 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Guegler, Karl J.
APPLICANT: Corley, Neil C.
APPLICANT: Gorgone, Gina
APPLICANT: Azimzai, Yalda
APPLICANT: Lu, Aina
                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Protein Kinase Homologs
FILE REFERENCE: PF-0614 US
CURRENT APPLICATION NUMBER: US/09/420,915
CURRENT FILING DATE: 1999-10-20
EARLIER APPLICATION NUMBER: US 09/173,581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Bandman, Olga
APPLICANT: Tang, Y. Tom
APPLICANT: Hillman, Jennifer L.
APPLICANT: Yue, Henry
                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: 119819
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                                                                                                                                               CAAGAGGACACCACGG 457
                                                                                                                                                                                CACTTCACGGAAGACATCCAGACTCGGCAGTACCGGGCCGTCGAGGTGCTGATCGGCGCC
                                                                                                                                                                                                             AAGGCCTGGAAGGACATCCGCCTGAGGACCGGACCCCAAGTTCGTTTGGCTGATCGGGGAC 441
                                                                                                                                                                                                                                                 AATGCAGATAAGATCAAGATCAAGATCGCAGACCTGGGCAACGCCTGCTGGGTGCACAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION:
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Search completed: December Job time: 52.0918 secs
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                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 58; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (650) 845-6504 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 1293 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Christopher L. Stone
REGISTRATION NUMBER: 35,696
REFERENCE/DOCKET NUMBER: GC38
TELECOMMUNICATION INFORMATION:
TELECHIONE: (650) 846-7555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: MUTANT THERMONOSPORA SPP. CELLULASE NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genencor International, Inc.
STREET: 925 Page Mill Road
                                                                                 1140 GGAACGGAAGATCGGGTGGACCAAGTGGAACTACTCGGAC 1179
                                                                                                                                                                1080 CTACACCGGTGACGGCCCAACGACTTCCAGATGGCCGACCGCTACATCGACCTGATGGC 1139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/924,440
FILING DATE: August 27, 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskett
                                                                                                                                                                                                        351 CTTCAATGCTGGCTGCAGCTACGTCCCCAAGAAGGCCTGGAAGGACATCCGCCTGAGGAC 410
                                                                                                                       411 GGACCCCAAGTTCGTTTGGCTGATCGGGGACCAAGAGGAC 450
                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
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TOPOLOGY: linear
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(650) 84
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                   9, 2002, 09:19:41
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Pred. No. 1.5;
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Result
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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Query
         Match
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| (Ggn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
| (Ggn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
| (Ggn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
| (Ggn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
| (Ggn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
| (Ggn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
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                                      /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.séq:*
/cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
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    US-09-905-114-1
US-09-905-114-3
US-09-905-134-3
US-09-952-436-336
US-09-954-456-271
US-09-980-107-3392
US-10-074-509-1
US-10-074-509-1
US-10-074-509-1
US-10-074-509-1
US-10-074-509-1
US-09-880-107-630
US-09-885-012-63
US-09-825-012-63
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Compugen Ltd
Sequence 1, Appli
Sequence 3, Appli
Sequence 316, App
Sequence 271, App
Sequence 3192, App
Sequence 1, Appli
Sequence 1, Appli
Sequence 11, Appli
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Db 267 CCCCTGCACCCCCTGAGACTCCGTTAGAGAGTTGATGACGCTGATGTCTAC 326 Oy 301 ACAGATGTGAAACGTCGCTGGAATTCATTTCATGGTGACTTCAATGCT 360 327 ACAGATGTGAAACGTCGCTGGAATGCAGAATTTCATTGGTGACTTCAATGCT 386 Oy 361 GGCTGCAGCTAGCTCGCTGGAATGCAGAATTTCATTTCA	## #PPLICANT: Soppet, Daniel ## #PPLICANT: Soppet, Daniel ## TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using S; ## TITLE OF INVENTION: Sets ## CURRENT APPLICATION NUMBER: US/09/962,436 ## PRIOR APPLICATION NUMBER: US/60/235,082 ## PRIOR APPLICATION NUMBER: US/60/235,082 ## PRIOR PILING DATE: 2000-09-25 ## PRIOR PILING DATE: 2000-09-25 ## PRIOR FILING DATE: 2000-09-25 ## SOFTWARE: PatentIn version 3.0 ## SEQ ID NO 336 ## LENGTH: 1023 ## TYPE: DNA ## ORGANISM: Homo sapiens US-09-962-436-336	Query Match 80.5%; Score 476.8; DB 10; Length 1023; Best Local Similarity 87.8%; Pred. No. 3.1e-140; Matches 520; Conservative 0; Mismatches 72; Indels 0; Gaps 0; Qy 1 GAGAGCTAAACGGAAATTCAAGAAAAGGCATAACATAAC	Db 241 GAGAAGCTGAAATTCAAGGAGGCATAACGTACTTTTTTTT	OY 301 ACAGATGTGAAACGTCGCTGGAATGCAGAGAATTTCATTTTCATGGGTGACTTCAATGCT 360
0y 181 GAACCCTTTGTGGTCCAGTCCACCCGACCCGTGCAAGGACTTCGTGATTGTC 240 bb 181 GAACCCTTTGTGGTCTGGTTCCAGTCACCCTACACCGCTGCTCAAGGACTTCGTGATTGTC 240 cccTGCACACCACCCCTGAGACACCCTTAGAGAGATTGATGAGCTGGTGATTGTCTAC 300 241 CCCCTGCACACCCCCTGAGACACTCGTTAGAGAGATTGATGATCTCATCTCA 300 0y 301 ACAGATGTGAAACCTCGTAGAGAATTTCATTTCATTGGTTCAATGCT 360 0y 301 ACAGATGTGAAACGTCGTGGAAGGAATTTCATTTTCATGGGTGACTTCAATGCT 360 0y 361 GGCTGCACATCGGGAAGCACTCGAAGGAATTCATTTCAT	RESULT 2 US-09-905-114-3 Sequence 3, Application US/09905114 Sequence 3, Application US/0905114 Sequence 3, Application US/0905114 Sequence 3, Application US/0905114 GENERAL INFORMATION: APPLICANT: ZHANG HUANMIN APPLICANT: BELLIN, MARY E TITLE OF INVENTION: ISOLATED POLYNUCLEOTIDE SEQUENCES ENCODING A FERTILITY ASSOCIATED CURRENT APPLICATION NUMBER: US/09/905,114 CURRENT FILING DATE: 2001-07-14 PRIOR PELLING DATE: 2000-07-14 PRIOR FILING DATE: 2000-07-14 NUMBER OF SEQ ID NOS: 9 SOFTWARE PATENTIN VERSION 3.1	100 08.	Best Local Similarity 100.0%; Pred. No. 1.3e-176; Best Local Similarity 100.0%; Pred. No. 1.3e-176; Best Local Similarity 100.0%; Pred. No. 1.3e-176; Batches 592; Conservative 0; Mismatches 0; Indels 0; Gagaccraaccgaaartcaacaccaraacaccaraccaccaccaccaccaccaccac	Db 207 GAACCCTTTGTGGTTCCAGTCACCCTACACCGCTGTCAAGGACTTCGTGATTGTC 266 Qy 241 CCCCTGCACACCCCTGAGACATCCGTTAGAGAGATTGATGACTGGCTGATGTCTAC 300

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CURRENT FILING DATE: 2001-09-18
PRIOR APPLICATION UNMBER: US/60/233,617
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: US/60/234,052
PRIOR FILING DATE: 2000-09-25
PRIOR PRIOR APPLICATION NUMBER: US/60/234,923
PRIOR FILING DATE: 2000-09-25
PRIOR FILING DATE: 2000-09-25
PRIOR APPLICATION NUMBER: US/60/235,134
PRIOR FILING DATE: 2000-09-25
PRIOR FILING DATE: 2000-09-25
PRIOR APPLICATION NUMBER: US/60/235,637
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PRIOR APPLICATION NUMBER: US/60/235,638
PRIOR FILING DATE: 2000-09-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 2276
SOFTWARE: PatentIn version 3.0
SEQ ID NO 271
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Best Local
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                                                                                                                                                                                                                                                             Matches 520;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Young, Paul TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Cancer TITLE OF INVENTION: Sets
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US/60/235,863 PRIOR FILING DATE: 2000-09-27
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                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 1023
TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                    Local Similarity
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                                                                                                                                                                                                  GAGAAGCTAAACGGAAATTCAAGAAAAGGCATAACATACAACTATGTGATTAGCTCTCGC 60
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                                  GTAAAACAAAGCTACCTCTACCACGACTATCAGGCTGGAGACGCAGATGTGTTTTCCAGG 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 3392
LENGTH: 1023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3392, Application US/09880107 Patent No. US20020142981A1
                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 3950
SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR FILING DATE: 2000-06-14
PRIOR APPLICATION NUMBER: US 60/237,054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Gene Expression Profiles
FILE REFERENCE: 44921-5028-WO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/880,107 CURRENT FILING DATE: 2001-06-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Horne, Darci T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                             241 GAGAAGCTGAACAGAAATTCAAGGAGAGGCATAACGTACAACTATGTGATTAGCTCTCGG 300
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                                                                                                                             CTTGGAAGAACACATATAAAGAACAGTATGCCTTTCTCTATAAAGAAAAAGCTAGTGTCT 120
                                                         GTAAAACAAAGCTACCTCTACCACGACTATCAGGCTGGAGACGCAGATGTGTTTTCCAGG 180
                                                                                                        CTTGGAAGAAACACATATAAAGAACAATATGCCTTTCTCTACAAGGAAAAGCTGGTGTCT 360
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                                   GTGAAGAGGAGTTATCACTACCATGACTATCAGGATGGAGACGCAGATGTTTTTCCAGG
                                                                                                                                                                                                                                                   520;
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Scherf, Uwe
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                                                                                                                                                                                                                                               Score 476.8; DB 10
Pred. No. 3.1e-140;
0; Mismatches 72;
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COMPUTER: 155 inch, 1.44 Mb floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/133,065
FILING DATE: 26-Apr-2002
CLASSIFICATION: -Unknown>
PRIOR APPLICATION: -Unknown>
PRIOR APPLICATION NUMBER: 09/43,520
FILING DATE: 22/08/2000
APPLICATION NUMBER: 09/794827
FILING DATE: 04-Feb-1997
APPLICATION NUMBER: 60/109796
FILING DATE: 05-Feb-1996
ATTORNEY/AGENT INFORMATION:
NAME: Evans, David W
REGISTRATION NUMBER: *See attached Limited Recognition under 37
REGISTRATION NUMBER: *See attached Limited Recognition under 37
                                                                                                                                                                                                                       099
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ACAGATGTGAAACGTCGCTGGAATGCAGAGAATTTCATTTTCATGGGTGACTTCAATGCT 360
                                                                                                                                                   ACGGACGTGAAACACCCCCGGAAGGCGGAGAATTTCATTTTCATGGGTGACTTCAATGCC 600
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                                                                       GGCTGCAGCTACGTCCCCCAAGAAGGCCTGGAAGAACATCCGCTTGAGGACTGACCCCAGG
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REFERENCE/DOCKET NUMBER: P1000R1C3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Baker, Kevin P.
Baron, Will F.
TITLE OF INVENTION: HUMAN DNASE
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
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TELEPHONE: 650/225-1739
TELEFAX: 650/952-9881
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Patent No. US20020123122A1
GENERAL INFORMATION:
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SEQUENCE CHARACTERISTICS:
LENGTH: 1079 base pairs
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STRANDEDNESS: Single
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COMPUTER READABLE FORM:
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US-10-133-065-1
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                                                                                                                            Indels
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APPLICATION NUMBER: US/10/074,509 FILING DATE: 11-Feb-2002
                                                                                      DB 12;
                                                                                  80.5%; Score 476.8; DB 12.
larity 87.8%; Pred. No. 3.2e-140;
Conservative 0; Mismatches 72;
7 TOPOLOGY: Linear
7 SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-133-065-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: HUMAN DNASE NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Genentech, Inc.
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CITY: South San Francisco
STATE: California
COUNTRY: USA
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Patent No. US20020142437A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Baker, Kevin P. Baron, Will F.
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COMPUTER READABLE FORM:
                                                                                  Query Match
Best Local Similarity
Matches 520; Conserv
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RESULT 8

US-10-133-065-11

; Sequence 11, Application US/10133065

; Patent No. US20020123122A1
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SEQUENCE CHARACTERISTICS:
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PRIOR APPLICATION UNMBER: 09/643,520
FILING DATE: 22/08/2000
APPLICATION NUMBER: 08/794827
FILING DATE: 04-Feb-1997
APPLICATION NUMBER: 08/1994827
FILING DATE: 05-Feb-1996
APPLICATION NUMBER: 60/109796
FILING DATE: 05-Feb-1996
ATTORNEY/AGENT INFORMATION:
NAME: JOHNSEON, Sean A.
REGISTRATION NUMBER: 35,910
REFERENCE/DOCKET NUMBER: 9100R1C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-3562
TELECHAN: 650/952-9881
                                                                                                                                                                                                                                                   707
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STRANDEDNESS: Single
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
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                                                                                                                           CTCGTCTTTGATTTCCAGAAAGCTTACAGGTTGTCTGAATCGAAGGCCCTGG 592
                                                                                                                                                                                               GTAAAACAAAGCTACCTCTACCACGACTATCAGGCTGGAGACGCAGATGTGTTTTTCCAGG
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                                                                                                       AGTGTTTTTGACTTCCAGAAAGCTTACAAGCTGACTGAAGAGGAGGCCCTGG
                                                                                                                                                                                                                                                                                                                    GGCTGCAGCTACGTCCCCAAGAAGGCCTGGAAGAACATCCGCTTGAGGACTGACCCCAGG
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                                                                                                                                                                                                                                                 TTTGTTTGGCTGATCGGGGACCAAGAGGACACCACGGTGAAGAAGAAGACACCAACTGTGCA
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TYPE: Nucleic Acid

STRANDEDNESS: Single
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-10-133-065-11
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Best Local Similarity
Matches 494; Conserv
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INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/10/133,065
FILING DATE: 26-Apr-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:

NAME: Evans, David W

REGISTRATION NUMBER: *See attached Limited Recognition under 37

C.F.R. 10.9(b)

REFERENCE/DOCKET NUMBER: Pl000R1C3
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Baron, Will F.
TITLE OF INVENTION: HUMAN DNASE
NUMBER OF SEQUENCES: 11
CONDECTORY.
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ADDRESSEE: Genentech, Inc
                                                                                          GAGCCCTTTGTGGTTTGGTTCCATTCCCCCCTTTACTGCTGTCAAGGACTTCGTGATTGTC
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                                 ACAGATGTGAAACGTCGCTGGAATGCAGAGAATTTCATTTCATGGGTGACTTCAATGCT 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 09/643,520 FILING DATE: 22/08/2000 APPLICATION NUMBER: 08/794827 FILING DATE: 04-Feb-1997 APPLICATION NUMBER: 60/109796 FILING DATE: 05-Feb-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: South San F
STATE: California
COUNTRY: USA
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Pred. No. 4.2
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CTTGGAAGAAACACATATAAAGAACAGTATGCCTTTCTCTATAAAGAAAAGCTAGTGTCT
                                            464 CTTGGAAGAACACGTACAAAGAGCAGTATGCCTTCGTCTACAAGGAGAAGCTGGTGTCT
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US-09-880-107-630
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APPLICANT: Scherf, Usee
APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
FILE REPERENCE: 4421-5028-WO
CURRENT APPLICATION NUMBER: US/09/880,107
CURRENT FILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR FILING DATE: 2000-06-14
PRIOR FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 3950
SOFTWARE: PALCHING VEY: 2.1
SEQ ID NOS: 3950
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Patent No. US20020142981A1
GENERAL INFORMATION:
APPLICANT: Horne, Darci T.
APPLICANT: Vockley, Joseph G.
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US-09-880-107-630/c
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: 1BM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genetech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/074,509
FILLING DATE: 11-Feb-2002
CLASSIFICATION: <unstraint of the companion of the companio
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Pred. No. 4.2e-127
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SEQUENCE DESCRIPTION: SEQ ID NO: 11:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Baron, Will F.
TITLE OF INVENTION: HUMAN DNASE
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genertech, Inc.
STREET: 1 DNA WAY
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Patent No. US20020142437A1
GENERAL INFORMATION:
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STRANDEDNESS: Single
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Best Local Similarity 83.4%;
Matches 494; Conservative
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COMPUTER READABLE FORM:
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331 AATTTCATTTTCATGGGTGACTTCAATGCTGGCTGCAGCTACGTCCCCAAGAAGGCCTGG 390
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                                                                                                                                        649 GCCGAGATCGACGCTCTCTATGACGTCTACCTGGATGTCCAAGAGAAATGGGGCTTGGAG
                                               589 TTCACAGAGGTCAGGGAGTTTGCCATTGTTCCCCTGCATGCGGCCCCCGGGGGACGCAGTA
                                                                                            271 AGAGAGATTGATGAGCTGGCTGATGTCTACACAGATGTGAAACGTCGCTGGAATGCAGAG
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Pred. No. 4.1e-37;
0; Mismatches 236; Indels
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APPLICANT: Young, Robert
TITLE OF INVENTION: Compounds for Targeting
FILE REFERENCE: 43191-256808
CURRENT APPLICATION NUMBER: US/09/825,012
CURRENT APPLICATION NUMBER: US 60/237,159
PRIOR APPLICATION NUMBER: GB 0008049.9
PRIOR PILING DATE: 2000-10-02
PRIOR PILING DATE: 2000-04
PRIOR FILING DATE: 2000-04
NUMBER OF SEQ ID NOS: 102
SOFTWARE: PatentIn version 3.1
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56.7%;
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ORGANISM: Homo sapiens
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Best Local Similarity
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US-09-825-012-2
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                   GATCGGGGACCAAGAGACACCACGGTGAAGAGAGCACCAACTGTGCATATGACAGGAT
                                                                272 TGTGCTTAGAGGACAAGAATCGTCAGTTCTGTTGCCCAAGTCAAACAGTGTTTTTTGA
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                                                                                                                                                            552 TITCCAGAAGCTTACAGGTTGTCTGAATCGAAGGCCCTGG 592
                                                                                                                                                                                        212 CTTCCAGAAAGCTTACAAGCTGACTGAAAAGGAGCCCTGG 172
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APPLICANT: Daugherty, Ann L.,
APPLICANT: Patapoff, Thomas W.
TITLE OF INVENTION: DNase Compaction Assay
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
21P: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
MEDIUM TYPE: TBM PC compatible
CAMPUTER: TBM PC compatible
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NAME: Glaister, Debra J.
REGISTRATION NUMBER: 33,888
REFERENCE/DOCKET NUMBER: 792
TELECOMMUNICATION INFORMATION:
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1039 bases
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APPLICATION NUMBER: 07/971,019
                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/09771078
Patent No. US20020034727A1
GENERAL INFORMATION:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
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STRANDEDNESS: single
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
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US-09-771-078-1
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US-09-825-012-4
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SEQ ID NO 4
SENGTH: 783
TYPE: DNA
ORGANISM: Homo sapiens
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Patent No. US20020122798A1
GENERAL INFORMATION:
APPLICANT: Young, Robert
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Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/825,012
CURRENT FILING DATE: 2001-04-03
PRIOR APPLICATION NUMBER: US 60/237,159
PRIOR FILING DATE: 2000-10-02
PRIOR APPLICATION NUMBER: GB 0008049.9
PRIOR FILING DATE: 2000-04-03
NUMBER OF SEQ ID NOS: 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Compounds for Targeting FILE REFERENCE: 43191-256808
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                     AATTTCATTTCATGGGTGACTTCAATGCTGGCTGCAGCTACGTCCCCAAGAAGGCCTGG 390
                                                                                                                                                                        TACACCGCTGTCAAGGACTTCGTGATTGTCCCCCTGCACACCCCCCGAGACATCCGTT 270
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GACGTCATGTTGATGGGCGACTTCAATGCGGGCTGCAGCTATGTGAGACCCTCCCAGTGG
                                                                                                         AGAGAGATTGATGAGCTGGCTGATGTCTACACAGATGTGAAACGTCGCTGGAATGCAGAG
                                                                                                                                               TTCACAGAGGTCAGGGAGTTTGCCCATTGTTCCCCTGCATGCGGCCCCGGGGGACGCAGTA
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Pred. No. 1.1e-36;
0; Mismatches 237;
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TITLE OF INVENTION: Compounds for Targeting
FILE REFERENCE: 43191-256808
CURRENT APPLICATION NUMBER: US/09/825,012
CURRENT FILING DATE: 2001-04-03
PRIOR APPLICATION NUMBER: US 60/237,159
PRIOR FILING DATE: 2000-10-02
PRIOR APPLICATION NUMBER: GB 0008049.9
PRIOR FILING DATE: 2000-04-03
NUMBER OF SEQ ID NOS: 102
SOFTWARE: Patentin version 3.1
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Matches
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ACCACGGTCAAGAAGAGCACAAACTGCGCCCTATGACAGGATCGTGCTTAGAGGACAAAAT
                                                                                                                                   GACGTCATGTTGATGGGCGACTTCAATGCGGGCTGCAGCTATGTGAGACCCCTCCCAGTGG
                                                                                                                                                                         AATTTCATTTCATGGGTGACTTCAATGCTGGCTGCAGCTACGTCCCCAAGAAGGCCTGG
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Pred. No. 1.2e-36;
0; Mismatches 237;
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  679 ACCACAGG---CTACACCCACGCACGCCTATGACAGGATCGTGGTTGCAGGGATGCTG 735
                                               511 ATTGTCAACTCTGGTGGTCCTCAATCAAACCTCGTCTTTGATTTCCAGAAAGCTTACAGG 570
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                                                                                           736 crccaagagacaricriccaacricagaricriraccirriaacrircaagaracciarge 795
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; OTHER INFORMATION: Humanised HMFG1 Fd - DNase I fusion
US-09-825-012-62
                                                                                                                                                                                                                                                  RESULT 15
US-09-825-012-62
Sequence 62, Application US/09825012
Patent No. US20020122798A1
GENERAL INFORMATION:
APPLICANT: Young, Robert
TITLE OF INVENTION: Compounds for Targeting
FILE REFERENCE: 43191-256808
CURRENT FILING DATE: 2001-04-03
PRIOR FILING DATE: 2001-04-03
PRIOR FILING DATE: 2000-10-02
PRIOR FILING DATE: 2000-10-02
PRIOR PILING DATE: 2000-10-02
PRIOR FILING DATE: 2000-04-03
NUMBER OF SEQ ID NOS: 102
SOFTWARE PATENTIN OF SEQ ID NOS: 102
SOFTWARE: PATENTIN OF SEQ ID NOS: 102
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ORGANISM: Artificial Sequence
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Best Local Similarity 56.5°
Matches 316; Conservative
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Db 1426 CTCCGAGGGGCGGTTGTTCCCGACTCGGCTTTTCCTTTAACTTCCAGGCTGCCTATGGC 1485
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Search completed: December 9, 2002, 09:24:07 Job time: 127.65 secs

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GenCore version 5.1.3 (c) 1993 - 2002 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a

AX329742 Sequence AX332286 Sequence AX332789 Sequence AX410746 Sequence U56814 Human DNase BC015831 Homo sapi AF047354 Homo sapi U75744 Homo sapien AF03985 Rattus no AX400016 Sequence
AK059612 Xenopus 1
AX407981 Sequence
AX001518 Bos tauru
AF311922 Bos tauru
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AX030575 Sequence
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AX068675 Sequence
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AX068679 Mus muscu
BC014718 Mus muscu Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G., Horrigan, S., Soppet, D.R. and Weaver, Z. Cancer gene determination and therapeutic screening using signature E11687 cDNA encodi U76110 Mus musculu AF047355 Mus muscu BC012671 Mus muscu PAT 09-JAN-2002 AX268721 Sequence
AX268722 Sequence
AX268702 Sequence
AX268703 Sequence
AX268729 Sequence
AX268739 Sequence
AX268739 Sequence
AX268739 Sequence
AX268730 Sequence
AX268703 Sequence Homo sapiens Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo AR047845 Sequence score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. Description linear DNA Sequence 251 from Patent WO0194629. AX329742. AX329742.1 GI:18102720 ALIGNMENTS SUMMARIES E11687 MMU76110 AF047355 BC012671 AR019468 BC014718 AX400016 AF059612 AF311922 AB041732 AB038776 D82875 AX030575 AX030591 AX268671 AX332789 AX410746 HSU56814 BC015831 6 AX407983 4 BTPANDNAI BC029437 HSA298844 AX268723 AX268729 AF047354 HSU75744 AF039852 RNU75689 HUMDNASE AR047845 AX268702 AX268730 AX330074 AX268701 AX268703 6 10 6 0110 6 10 10 DB 1039 Length 1023 1023 1023 1023 1023 1023 1108 1108 11108 11108 11208 1208 1283 1210 1161 1039 1039 1312 1337 1548 Query Match 481.2 474.8 474.8 473.2 411.4 298.4 195.6 195.6 182.4 181.4 173.8 172.6 164.8 163.2 163.2 163.2 163.2 161.6 161.6 DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS RESULT 1 AX329742 TITLE Result No. LOCUS

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Patent: WO 0194629-A 251 13-DEC-2001;
Avalon Pharmaceuticals (US)
Location/Qualifiers
Young, P.E.,
Horrigan, S.,
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 Augustus, M., Soppet, D.R.
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Pred. No. 1.1e-132;
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1t WO0194629
 Carter, K.C., and Weaver, Z.
                                        Craniata; Vertebrata;
Catarrhini; Hominidae;
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REFERENCE AUTHORS

Young, P.E.,

Augustus, M.,

Carter, K.C.,

Ebner, R.,

SOURCE ORGANISM

Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae

Euteleostomi;

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/db_xref="taxon:9606"
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Pred. No. 1.1e-132;
0; Mismatches 80;
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and Vockley, J.G.

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Horrigan, S., Soppet, D.R. and Weaver, Z. Cancer gene determination and therapeutic gene sets. WO 0194629-A 3298 13-DEC-2001;
                                                                                                                                         Score 527; DB 6;
Pred. No. 1.1e-132;
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                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                               Avalon Pharmaceuticals (US)
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

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1023 bp mRNA linear PRI 24-JUL-1997 protein (DNAS1L3) mRNA, complete cds.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 1.1e-132;
0; Mismatches 80; Indels
                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
/note="EMBL/GenBank Accession No.
1 244 c 240 g 227 t
Alvares, C., Horne, D., Peres-da-Silva, S. a
Gene expression profiles in liver cancer
Patent: WO 0229103-A 3393 11-APR-2002;
GENE LOGIC INC (US)
Location/Qualifiers
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                          ACATCCGCCTGAGGACGGACCCCAAGTTCGTTTGGCTGATCGGGGACCAAGAGGACACCA 480
                                                                                                         TCATTTTCATGGGTGACTTCAATGCTGGCTGCAGCTACGTCCCCAAGAAGGCCCTGGAAGG 420
                                                                                                                                                                                                                                                                       CCGCTGTCAAGGACTTCGTGATTGTCCCCCTGCACACCACCCCTGAGACATCCGTTAGAG
                                                                                                                                                                                                                                                                                                                                                    CTGGAGACGCAGATGTGTTTTCCAGGGAACCCTTTGTGGTCTGGTTCCAGTCACCCCTACA 240
                                                                                                                                                                                                 AGATTGATGAGCTGGCTGATGTCTACACAGATGTGAAACGTCGCTGGAATGCAGAGAATT 360
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                                                                              TCATTTTCATGGGTGACTTCAATGCCGGCTGCAGCTACGTCCCCAAGAAGGCCTGGAAGA 634
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Schneider, M.C. and R
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (25-APR-1996) M.C. Schneider,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="DNase1-Like III protein"
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SVKEIDELVEVTTDVKHENKARMFIFTMGDFNGCSYVPKKAWKNIRLETDERFVWLTD
SVKEIDELVEVTTDVKHENKARMFIFTMGDFNGVHGDG
QCDTTVKKSTNCAYDRIVLRGQBIVSSVVPKSNSVFDFQKAYKLTEEEALDVSDHFP
VEFKLQSSRAFTNSKKSYTLRKKTKSKKS"
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25. .942
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/clone lib="Stratagene liver (#937224)"
/note="corresponds to EST clones 8226 (GenBank Accession Number T69965), 82738 (GenBank Accession Number T73558, T73653), 78422 (GenBank Accession Number T61400,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         T61368
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/db_xref="taxon:9606"
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87.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Clone distribution: MGC clone distribution information can be four through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 38 Row: p Column: 7
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA g1: 4826697
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cDNA Library Preparation: CLONTECH Laboratories, IncDNA Library Arrayed by: The I.M.A.G.E. Consortium DNA Sequencing by: Institute for Systems Biology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CLONTECH
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Submitted (15-OCT-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genemics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   contact: amadan@systemsbiology.org
Anup Madan, Rachel Dickhoff, Jessica Fahey,
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                                                                                    /translation="MSRELAPLLLLLSIHSALAMRICSFNVRSFGESKQEDKNAMDVIVKVLKCDIILVMEIKDSNNRICFILMEKLMRNSRRGITYNVVISSRLGRNTYKEQYAFLYKEKLYSVKRSYHYNYQDGDADVFSREFEVVNFOSPHTAVKDFVIIFLHFTTPETSVKELLSVKRSYHYNYQDGDADVFSREFEVVNFOSPHTAVKDFVIILDHTTPETSVKELLSVKRSYHYNYQDGDADVFSREFEVVNFOSPHTAVKDFVIILDHTTPETSVKELLSVKRSYHYNYQDGDADVFSREFEVNFOSPHTAVKDFVILLG
                                           DQEDTTVKKSTNCAYDRIVLRGQEIVSSVVPKSNSVFDFQKAYKLTEEEALDVSDHFP
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                                                                                                                                                                                /product="deoxyribonuclease I-like
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                      /codon_start=1
                                                                                                                                                                                                                                                                                                                                           tissue_type="Liver"
/clone_lib="NIH_MGC_76"
                                                                                                                                                                                                                                                                                                                          lab_host="DH10B"
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mRNA, complete
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cloning and characterization of an actin-resistant DNase I-like endonuclease secreted by macrophages Gene 215 (2), 291-301 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 (bases 1 to 1079)
Baron,W.F., Pan,C.Q., Spencer,S.A., Ryan,A.M., Lazarus,R.A. and
Baker,K.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and
                                                                                                                                                                                378 TTCTCTACAAGGAAAAGCTGGTGTCTGTGAAGAGGAGTTATCACTACCATGACTATCAGG 437
                                                                                                                                                                                                                      CTGGAGACGCAGATGTGTTTCCAGGGAACCCTTTGTGGTCTGGTTCCAGTCACCCTACA 240
                                                                                                                                                                                                                                                                                                                                                                                                      258 ACAACAGGATCTGCCCCATACTGATGGAGAAGCTGAACAGAAATTCAAGGAGAGGGGCATAA 317
                                                                                                           CATACAACTATGTGATTAGCTCTCGCCTTGGAAGAACACATATAAAGAACAGTATGCCT 120
                                                                                                                                      CGTACAACTATGTGATTAGCTCTCGCCTTGGAAGAACACATATAAAGAACAATATGCCT 377
                                                                                                                                                                                                                                    CCGCTGTCAAGGACTTCGTGATTGTCCCCCTGCACACCCCCTGAGACATCCGTTAGAG 300
                                                                                                                                                                                                                                                                                          CTGCTGTCAAAGACTTCGTGATTATCCCCCTGCACACCACCCCAGAGACATCCGTTAAGG 557
                                                                                                                                                                                                                                                                                                                               AGATTGATGAGCTGGCTGATGTCTACACAGATGTGAAACGTCGCTGGAATGCAGAGATT 360
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                             Gaps
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1 (bases 1 to 1079)
Baron, W.F., Pan, C.Q., Spencer, S.A., Ryan, A.M., Lazarus, R.A.
Baker, K.P.
                                                                                                                                                                TTCTCTATAAAGAAAAGCTAGTGTCTGTAAAACAAAGCTACCTCTACCACGACTATCAGG
                                                     1 ACAACAGGATCTGCCCCATACTGATGGAGAAGCTAAACGGAAATTCAAGAAAAGGCATAA
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  Length 1067;
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                             80; Indels
Score 527; DB 9; I
Pred. No. 1.1e-132;
0; Mismatches 80;
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 Query Match
Best Local Similarity 87.8%;
Matches 575; Conservative
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 Query Match
Best Local 8
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AUTHORS
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/codon_start=1
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/protein_id="AAGC35752.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                IVKVIKRCDI ILVYBI KDSNNR I CPI LMEKLINRNSRRGI TYNYVI SSRLGRNTYKEQY
RELYKEKLOSSYKRŠYHYHDYODGADAPVERREPYVWRQOSPHTAVKDEV I BLHTTPET
SVER I DELVEVYTDYKRKRIKKARNET FINGDRRAGCS VV PKKARKNI FLRTDPR FVWL I G
DQEDTTVKKSTNCAYDR I VLRGQE I VSSVVPKSNSVFDFQKAYKLTEEFALDVSDHFP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CATACAACTATGTGATTAGCTCTCGCCTTGGAAGAACACATATAAAGAACAGTATGCCT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                261 ACAACAGGATCTGCCCCATACTGATGGAGGCTGAACAGAAATTCAAGGAGAGAGGCATAA 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
Direct Submission
Submitted (09-FEB-1998) Molecular Biology, Genentech Inc., 1
Way, South San Francisco, CA 94080, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ACAACAGGATCTGCCCCATACTGATGGAGAAGCTAAACGGAAATTCAAGAAAAGGCATAA
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87.8%; Pred. No. 1.1e-132;
ive 0; Mismatches 80; Indels
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260 c 252 q 237 t
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                                                                                                       1. 1079
/organism="Homo sapiens"
/db_xref="taxon:9606"
1. _1079
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/qene="LSD"
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/gene="LSD"
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                          CCGCTGTCAAGGACTTCGTGATTGTCCCCCTGCACACCACCCCCTGAGACATCCGTTAGAG 300
                                                                                          CTGGAGACGCAGATGTGTTTTCCAGGGAACCCTTTGTGGTCTGGTTCCAGTCACCCTACA 240
                                                                                                                                                                                                                                                                          ACAACAGGATCTGCCCCATACTGATGGAGAAGCTGAACAGAAATTCAAGGAGAGGCATAA 342
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   CTGCTGAAAGACTTCGTGATTATCCCCCCTGCACACCACCCCAGAGACATCCGTTAAGG
                                                                                                                                       TTCTCTACAAGGAAAAGCTGGTGTCTGTGAAGAGGAGTTATCACTACCATGACTATCAGG 462
                                                                                                                                                              TTCTCTATAAAGAAAAGCTAGTGTCTGTAAAACAAAGCTACCTCTACCACGACTATCAGG 180
                                                                                                                                                                                                          CGTACAACTATGTGATTAGCTCTCGGCTTGGAAGAAAAACATATAAAGAACAATATGCCT
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2. (bases 1 to 1108)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (23-OCT-1996) Biochemistry, Science Univ. of Tokyo.
Shinjuku-ku Ichigaya Funagawaracho, Tokyo 162, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shiokawa, D. and Tanuma, S. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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VEFKLQSSRAFTNSKKSVTLRKKTKSKRS"
1 261 c 271 g 247 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="DNase gamma"
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     function="deoxyribonuclease"
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                                                                                                                                                                                                                                                                                                                                                              78.3%;
87.6%;
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                                                                                                                                                                                                                                                                                                                                              Score 525.4; DB 9;
Pred. No. 3.1e-132;
0; Mismatches 81;
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AF039852
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Liu,Q.Y., Singh,R.K., Lin,W.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                     Submitted (24-DEC-1997) Institute for Research Council, 1200 Montreal Road,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sikorska,M.
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Mammalia; Eutheria;
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                                                                          /protein_id="AAC28937.1"
/db_xref="GI:3395772"
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/transletion="MSLYPAGPYLASLLLFILALHGALSLRLCSFNVRSFGESKKENH
/translrikitkcollilmeikdsnnnicpmlmeklngnsrsttynyvissrlgrnt
VKEQYAFLYKEKLVSVKAKYLYHDYQDGDTDVFSREDFVVWFQAFTAAKDFVIVPLH
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/strain="Sprague-Dawley"
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Rodentia;
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  J. 332 (Pt 3), 713-720 (1998)
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Shiokawa, D. and Tanuma, S.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
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               Length 1331;
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Shiokawa, D., Ohyama, H., Yamada, T., Takahashi, K.
Identification of an endonuclease responsible f
thymocytes
            Score 501.4; DB 10;
Pred. No. 1.1e-125;
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Shlokawa, D. and Tanuma, S.
Molecular cloning and expression of a
endonuclease DNase gamma
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Direct Submission
Submitted (22-OCT-1996) Biochemistry, Science Univ. of
Shinjuku-ku ichigaya funagawaracho, Tokyo 162, Japan
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larity 85.3%; Pred. No. 1.1e-125;
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                                                      TCAACTCTGTGGTTCCCCGCTCCAGTGGCGTCTTTGACTTTCAGAAAGCTTATGAGTTGT
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Location/Qualifiers
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llarity 85.1%;
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                                                                                          TTCTCTATAAAGAAAAGCTAGTGTCTGTAAAACAAAGCTACCTCTACCACGACTATCAGG 180
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CCGCTGTCAAGGACTTCGTGATTGTCCCCCCTGCACACCCCCTGAGACATCCGTTAGAG
                                        CTGGAGACGCAGATGTGTTTTCCAGGGAACCCTTTGTGGTCTGGTTCCAGTCACCCCTACA
                                                                          TCCTCTACAAGGAGAAGCTGGTGTCTGTGAAGGCAAAATACCTCTACCATGACTATCAGG
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TANUMA YASUKAZU
OS Rattus rattus (rat)
PN JP 1996187079-A/1
PD 23-JUL-1996
PF 06-SEP-1994 JP 94P 2
PI TANUMA YASUKAZU
PC C12N9/16,CO7K14/47,CO7
C12R1:19);
CC strandedness: Double;
CC topology; Linear;
CC topology; Linear;
CC hypothetical: No;
CC anti-sense: No;
FH Key Locati
FH Key 1. 1.2
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Mammalia; Eutheria;
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JP 1996187079-A/1
23-JUL-1996
06-SEP-1995 JP 1995255647
06-SEP-1994 JP 94P 239518
TANUMA YASUKAZU
C12N9/16,C07K14/47,C07K16/40,C12N1/21,C12N15/09,(C12N1/21,
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5'UTR
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85.1%;
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Rodentia;
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/tissue_type='Thymus, Spl
nucleus'
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Pred. No. 3.5e-120;
0; Mismatches 93;
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which cut
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Mus musculus liver and spleen DNase precursor (LSD) mRNA, complete
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Baron, W.F., Pan, C.Q., Spencer, S.A., Ryan, A.M., Lazarus, R.A. and Baker, K.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cloning and characterization of an actin-resistant DNase I-like
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Baron,W.F., Pan,C.Q., Spencer,S.A., Ryan,A.M., Lazarus,R.A.
Baker,K.P.
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   ATACAACTATGTGATTAGCTCTCGCCTTGGAAGAACACATATAAAGAACAGTATGCCTT
                                                                               122 TCTCTATAAAGAAAAGCTAGTGTCTGTAAAACAAAGCTACCTCTACCACGACTATCAGGC
                                                                                                                     333 CGTCTACAAGGAGAAAGCTGGTGTCTGTGAAGACAAAATACCACTACCATGACTATCAGGA
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/db_xref="taxon:10090"
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/produCt="DNase gamma"
/produCt="DNase gamma"
/produCt="DNase gamma"
/produCt="AAD09222.1"
/db xref="GI:4098208"
/trānslation="MSLHPASPRLASLILFILALHDTLALRLCSFNVRSFGASKKENH
Kranslation="MSLHPASPRLASLILFILAHDTLALRLCSFNVRSFGASKKENH
EAWDIIVKIIKRCDLILLMEIKDSSNNICPWLMEKLNGNSRSTTYNYVISSRLGRNT
YKEQYAFVYKEKLVSVKTKYHYHDYQDGDTDVSRREPFVVWFRSPFTAVKDFVIVPLH
TTPETSVKEIDELVDVYTNDRSQWKTENFIPMCDFNAGCSYVPKAAWONIRLATDPKF
VWLIGDQEDTTVKKSTSCAYDRIVLCGQEIVNSVVPRSSGVFDFQKAYDLSEEEALDV
SDHFPVEFKLQSSRATNNRKSVSLKKRKKGNRS"

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Shiokawa, D., Hatanaka, T. and Tanuma, S.
Direct Submission
Submitted (24-0CT-1996) Biochemistry, Science Univ. of Tokyo, Shinjuku-ku ichigaya tunagawaracho, Tokyo 162, Japan
Location/Qualifiers
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AGATAGATGGATGGCTGGCTGTCTACACGGATGTTAGAAGACGATGGAGGCAGAGTTT
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Pred. No. 1.9e-118;
0; Mismatches 112;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1. .941
/organism="Mus musculus"
/strain="C57 black"
/db_xref="taxon:10090"
7. .939
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/function="apoptosis"
/note="deoxyribonuclease"
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Mus musculus DNase gamma mRNA, c
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llarity 82.9%;
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                   TGAATCGAAGGCCCTGGATGTCAGCGACCACTTTCCAGTTCATCATCATCATCA 655
                                                                                             CAACTCTGGTGGTCCTCAATCAAACCTCGTCTTTGATTTCCAGAAAGCTTACAGGTTGTC
                                                                                                                                                           GGTCAAGAAGAGCACAAACTGCGCCTATGACAGGATCGTGCTTAGAGGGACAAAATATTGT
                                                                                                                                                                                                      CATTCGTTTGAGGACGGACCCCAAGTTTGTTTGGCTGATTGGGGACCAAGAGGACACTAC
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                                                                                                                                                                                                                                                                                                         CATTTTCATGGGTGACTTCAATGCTGGCTGCAGCTACGTCCCCAAGAAGGCCTGGAAGGA 421
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TGAGGAGGAGGCCCTGGATGTCAGTGATCACTTTCCAGTTGAGTTTAAGCTACA 1032
                                                                   CAACTCCGTGGTTCCCCGTTCCAGTGGCGTCTTTGACTTTCAGAAAGCTTATGACTTGTC
                                                                                                                                    GGTCAAGAAGAGTACCAGCTGTGCCTATGACAGGATTGTGCTTTGTGGACAAGAGATAGT
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/product="liver and spleen
/protein_id="AAC35753.1"
/db_xref="GI:2905788"
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/evidence=not
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/note="actin
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                                                                                                                                                                                                                                                           Local Similarity
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TCTCTATAAAAAAGCTAGTGTCTGTAAAACAAAGCTACCTCTACCACGACTATCAGGC
                                                                  ATACAACTATGTGATTAGTTCTCGACTTGGAAGAACACGTACAAAGAGCAGTATGCCTT
                                                                                                                                                      CAACAACATCTGTCCCATGCTGATGGAGAAGCTGAATGGAAATTCACGAAGAAGCACAAT 416
                                                                                                                                                                                                CAACAGGATCTGCCCCATACTGATGGAGAAGCTAAACGGAAATTCAAGAAAAGGCATAAC 61
                                                                                                            ATACAACTATGTGATTAGCTCTCGCCTTGGAAGAAACACATATAAAGAACAGTATGCCTT
                                                                                                                                                                                                                                          541;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 18 Row: 1 Column: 14
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 668120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium
DNA Sequencing by: Institute for Systems Biology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             contact: amadan@systemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman,
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (15-AUG-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus, Similar to deoxyribonuclease 1-like MGC:13854 IMAGE:4160709, mRNA, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Clone distribution: MGC clone distribution information can be found
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           http://www.systemsbiology.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota;
Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Institute, 31 Center Drive, Room 11A03, Bethesda, MD
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Location/Qualifiers
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EAMDIIVKIITRCDLILLMEIKDSSNNICPMLMEKLNGNSRSFIYNYVISSRLGRNIT 
YKEQZAFVYKEKLVSVKTKYHYDQQGDTDVFSREPFVVWFHSPFTAVKDFVIVPLH 
TTPETSVKEIDELUDVYTDVRSQWKTENFIFMGDFNAGCSYVPKKAMQNIRLRTDPKF 
VMLIGDQEDTTVKKSTSCAYDRIVLCGQEIVNSVVPRSSGVFDFQKAYDLSEEEALDV 
SDHFPVEFKLQSSRAFTNNRKSVSLKKRKKGNRS" 
581 c 464 g 539 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=1
/product="Similar to deoxyribonuclease 1-like
/protein_id="AAH12671_1"
/db_xref="GI:15215119"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="Liver, normal.
/clone_lib="NCI_CGAP_Li9"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="MGC:13854 IMAGE:4160709"
/tissue_type="Liver, normal. 5 m
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                                    302 GATTGATGAGCTGGCTGATGTCTACACAGATGTGAAACGTCGCTGGAATGCAGAGAATTT 361
                                                                                                                                                                  CATTITICATGGGTGACTICAATGCTGCTGCAGCTACGTCCCCAAGAAGGCCTGGAAGGA 421
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The invention relates to bovine fertility associated antigen (FAA) and cits nucleic acid sequence. FAA is useful for increasing the stability of the plasma membrane plus acrosome of a sperm cell and/or other portions of a sperm cell, in particular mammalian sperm cell such as a sperm cell from buffalo, cow, horse, mice, pig, sheep, human, avian sperm cell including turkey or chicken sperm cell. FAA is also useful for increasing the fertility of sperm from a mammal including buffalo, cow, horse, mice, pig, sheep or human, or avian (chicken or turkey). FAA is added to the suspension of sperm cells prior to preservation or prior to administration of the sperm cells to a mammal in artificial insemination. Alternatively, fertility of sperm from a mammal is increased by placing calls into the female's reproductive tract by coppulation or artificial insemination. The fertility of the male mammal is increased by injecting faAA into the male mammal's reproductive tract. The present sequence is bovine 22kDa recombinant FAA (rFAA) coding sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1;
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                                                                                                                                                                                                 TCAACTCTGGTGGTCCTCAATCAAACCTCGTCTTTGATTTTCCAGAAAGCTTACAGGTTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCATTTTCATGGGTGACTTCAATGCTGGCTGCAGCTACGTCCCCAAGAAGGCCTGGAAGG 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGATTGATGAGCTGGCTGATGTCTACACAGATGTGAAACGTCGCTGGAATGCAGAGAATT
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AAGAACCATGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCGCTGTCAAGGACTTCGTGATTGTCCCCCCTGCACCACCCCCTGAGACATCCGTTAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTGGAGACGCAGATGTTTTTCCAGGGAACCCTTTGTGGTCTGGTTCCAGTCACCCTACA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTGGAGACGCAGATGTGTTTTCCAGGGAACCCTTTGTGGTCTGGTTCCAGTCACCCTACA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTCTCTATAAAGAAAAGCTAGTGTCTGTAAAACAAAGCTACCTCTACCACGACTATCAGG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CATACAACTATGTGATTAGCTCTCGCCTTGGAAGAAACACATATAAAGAACAGTATGCCT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACAACAGGATCTGCCCCATACTGATGGAGAAGCTAAACGGAAATTCAAGAAAAGGCATAA 60
                                                  CTGAATCGAAGGCCCTGGATGTCAGCGACCACTTTCCAGTTCATCATCATCATCATCATG
                                                                                                 CTGAATCGAAGGCCCTGGATGTCAGCGACCACTTTCCAGTTCATCATCATCATCATCATG
                                                                                                                                                         TCAACTCTGGTGGTCCTCAATCAAACCTCGTCTTTGATTTCCAGAAAGCTTACAGGTTGT
                                                                                                                                                                                                                                                                                                                         CGGTCAAGAAGAGCACAAACTGCGCCTATGACAGGATCGTGCTTAGAGGACAAAATATTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCATTTTCATGGGTGACTTCAATGCTGGCTGCAGCTACGTCCCCAAGAAGGCCTGGAAGG
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Pred. No. 4e-202;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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RESULT 2
AAD29088
В
                                                                                                                                                                                         Novel amino acid and polynucleotide sequence for fertility associated antigen useful for increasing stability of plasma membrane, acrosome and other portions of sperm cell, and increasing fertility of mammals
                                                                                                                                                                  Claim 1; Fig 6; 37pp; English.
                                                                                                                                                                                                                              P-PSDB; AAE18281
                                                                                                                                                                                                                                       WPI; 2002-171803/22.
                                                                                                                                                                                                                                                                                                           16-JUL-2001; 2001WO-US22097
                                                                                                                                                                                                                                                                                                                                             WO200206444-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                          reproductive
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bovine; fertility associated antigen; FAA; artificial insemination; plasma membrane; s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bovine fertility associated antigen (FAA) partial cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAD29088;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAD29088 standard; cDNA; 592
                                                                                                                                                                                                                                                       Zhang H,
                                                                                                                                                                                                                                                                         (ARIZ-)
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                                                                                                                                                                                                                                                       Ax RL,
                                                                                                                                                                                                                                                                                                                                                                                                                                           tract; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first
                                                                                                                                                                                                                                                                                                                                                                   /*tag= a
/product= "Bovine fertility associated antigen (FAA)"
/note= "CDS does not include start and stop codon"
                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
1..591
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                                                                                                                                                                                                                                                       Bellin ME;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entry.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                  sperm fertility; acrosome;
sperm cell; anti-infertility;
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its nucleic acid sequence. FAA is useful for increasing the stability of the plasma membrane plus acrosome of a sperm cell and/or other portions of a sperm cell, in particular mammalian sperm cell such as a sperm cell crom buffalo, cow, horse, mice, pig, sheep, human, avian sperm cell from buffalo, cow, horse, mice, pig, sheep, human, avian sperm cell concluding turkey or chicken sperm cell. FAA is also useful for increasing the fertility of sperm from a mammal including buffalo, cow, horse, mice, pig, sheep or human, or avian (chicken or turkey). FAA is added to the conclusion of sperm cells prior to preservation or prior to administration of the sperm cells to a mammal in artificial insemination. Alternatively, fertility of sperm from a mammal is increased by placing FAA into a female's reproductive tract prior to deposition of the sperm cells into the female's reproductive tract by copulation or artificial consemination. The fertility of the male mammal is increased by injecting FAA into the male mammal's reproductive tract. The present sequence is bovine fertility associated antigen (FAA) partial cDNA. invention relates to bovine fertility associated antigen (FAA)

Sequence 592 BP; 170 A; 143 C; 142 G; 137 T; 0 other;

Query Match Best Local Sin Matches 592; Similarity 88.2%; Sur 100.0%; Pr Score 592; DB; Pred. No. 4.1.
0; Mismatches 4.1e-177; DB 24; Length

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27 GAGAAGCTAAACGGAAATTCAAGAAAAGGCATAACAACTATGTGATTAGCTCTCGC 86

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18-OCT-2001.

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Fertility-associated antigen; FAA; antiinfertility; sperm cell acrosome, reproductive fitness; single nucleotide polymorphism; SNP; bovine; cow;
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                                                                                                                                                                      TTCGTTTGGCTGATCGGGGACCAAGAGGACACCACGGTCAAGAAGAGAGCACAACTGCGCC
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                                                                               GTAAAACAAAGCTACCTCTACCACGACTATCAGGCTGGAGACGCAGATGTGTTTTCCAGG
                                                                                          GTAAAAACAAAGCTACCTCTACCACGACTATCAGGCTGGAGACGCAGATGTGTTTTCCAGG
                                                                                                                                          GAACCCTTTGTGGTCTGGTTCCAGTCACCCTACACGCTGTCAAGGACTTCGTGATTGTC
                                                                                                                                                                                            ccccrdcacacacccrdagacarccgrragagagarrgargagacrgargrcrac
                                                                                                                                                                                                                                                                 GGCTGCAGCTACGTCCCCAAGAAGGCCTGGAAGGACATCCGCCTGAGGACGCCCCAAG
                                                                                                                                                                                                                                                                                      CTTGGAAGAACACATATAAAGAACAGTATGCCTTTCTCTATAAAGAAAAGCTAGTGTCT
                                                                                                                          GAACCCTTTGTGGTCTGGTTCCAGTCACCCTACACGCTGTCAAGGACTTCGTGATTGTC
                                                                                                                                                                                                                    ACAGATGTGAAACGTCGCTGGAATGCAGAATTTCATTTTCATGGGTGACTTCAATGCT
                                                                                                                                                                                                                                         TTCGTTTTGGCTGATCGGGGACCAAGAGGACACCACGGTCAAGAAGAGAGCACAAACTGCGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /transl_except= (pos:325..326, aa:R)
/note= "This codon has an apparent 1 nucleotide
deletion which alters the reading frame"
/transl_except= (pos:576..579, aa:RLSESKAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "No start or stop codon given"
/transl_except= (pos:289..300, aa:A)
/note= This codon has an apparent 9 nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                   CTCGTCTTTGATTTCCAGAAGCTTACAGGTTGTCTGAATCGAAGGCCCTGG 618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA encoding bovine fertility-associated antigen (FAA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product= "FAA"
/note= "Fertility-associated antigen"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  insertion"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAS17900 standard; cDNA; 578 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "FAA"
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WO200176529-A2

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The invention describes a novel isolated human fertility-associated antigen (FAA) and a bovine FAA polypeptide. Human or bovine FAA is useful for increasing the stability of a sperm cell acrosome and for increasing the stability of a sperm cell acrosome and for increasing the fertility of a human male by administering FAA. Detecting single nucleotide polymorphisms (SNPs) of the human or bovine FAA gene is useful to rasaying fertility by detecting the presence or absence of a FAA SNP con the mammal and correlating the presence or absence of a FAA SNP con the mammal. The FAA SNPs are chosen from FAA SNPs 1-34 given in the specification. FAA SNP is also useful for determining the reproductive citication. FAA SNP is also useful for determining the reproductive citication or bovine, by determining the nucleotide sequence of the FAA SNP, quantifying the fertility of more than one mammal containing creamproductive fitness of the mammals. FAA improves the integrity of sperm membranes and increases the capacitation of sperm derived from either configuration infertile humans. Barly genetic identification of infertility improves the prognosis for subsequent attempts at fertilisation and featility from fertility treatments to avoid costly and/or employed the house of the first first from fertility treatments to avoid costly and/or employed.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTCAATGCTGGCTGCAGCTACGTCCCCAAGAAGGCCTGGAAGGACATCCGCCTGAGGACG 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                Novel human or bovine fertility-associated antigen useful for stabilising sperm cell acrosome and increasing fertility of a male
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GAGAAGCTAAACGGAAATTCAAGAAAAGGCATAACATACAACTATGTGATTAGCTCTCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                87 CTTGGAAGAAACACATATAAAGAACAGTATGCCTTTCTCTATAAAGAAAAGCTAGTGTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 GTAAAACAAAGCTACCTCTACCACGACTATCAGGCTGGAGGCGCAGATGTTTTTCCAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GATGTCTACACAGATGTGAAACGTCGCTGGAATGCAGAGAATTTCATTTCATGGGTGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27 GAGAAGCTAAACGGAAATTCAAGAAAAGGCATAACATACAACTATGTGATTAGCTCTCGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAACCCTTTGTGGGTCTGGTTCCAGTCACCCTACACGCTGTCAAGGACTTCGTGATTGTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         problems with attempted inseminations. This sequence encodes the lettility-associated antigen (FAA) described in the method of the
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                                                                                                                                                                                                                                                                                                                                              Claim 25; Fig 2A-E; 54pp; English.
                                      09-APR-2001; 2001WO-US10802.
                                                                              07-APR-2000; 2000US-195225P.
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                                                                                                                    ZHAN/) ZHANG H M.
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                                                                                                     The invention relates to a novel method for diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma or metastatic liver tumour in a patient, and differentiating metastatic liver cancer from hepatocellular carcinoma in a patient, involving detecting the level of expression of two or more genes represented in ABN93503-ABN97455 in a cissue sample. The method of the invention has hepatotropic, and cytostatic activity. The method is useful for diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma and metastatic liver carcinoma in a patient. The method is useful for identifying expression profiles which serve as useful diagnostic markers as well as markers that can be used to monitor disease states, disease progression, of drug toxicity, drug efficacy and drug metabolism.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
 Query Match
Best Local S
Matches 575
                                                                                                                                                                                                                                                                                                                                                                                             Diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma or metastatic liver tumor in a patient, involves detecting the level of expression of two or more genes
                                                                Sequence 1023
                                                                                                                                                                                                                                                                                                                                                    Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gene; liver cancer; ds; hepatocellular carcinoma; hepatotropic; metastatic liver tumour; cytostatic; expression profile; disease state; disease progression; drug toxicity; drug efficacy; drug metabolism.
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                                                                BP; 312 A; 244 C; 240 G;
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 Score 527; DB 24;
Pred. No. 2.2e-156;
D; Mismatches 80;
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05-JUN-2000; 2000US-209473P.
05-JUN-2000; 2000US-209531P.
18-SEP-2000; 2000US-233133P.
18-SEP-2000; 2000US-233617P.
                                                                                                                                                                         cytostatic;
gene; ds.
                                                                                                                                                                                Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid; stomach; lung; prostate; pancreas; carcinoma; antitumour; cancero cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocar
                                                                30-MAY-2001;
                                                                                          13-DEC-2001.
                                                                                                                                                                                                                                        Colon
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                                                                                                                                                                                                                                                                                                                     ABL61914 standard;
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                                                                                                                                                                                                                                       adenocarcinoma
                                                                2001WO-US10838
                                                                                                                                                                                                                                                                 (first entry)
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                                                                                                                                                                                                                                        related
                                                                                                                                                                                                                                       gene sequence
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                                                                                                                                                                                    tumour; adenocarcinoma;
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87.8%; Pred. No. 2.2e-156;

Best Local Similarity

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Query Match
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78.5%; Score 527; DB 24; Length 1023;

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ΚĊ,
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                  22-SEP-2000; 2000US-234509P.

25-SEP-2000; 2000US-234567P.

25-SEP-2000; 2000US-234524P.

25-SEP-2000; 2000US-23577P.

25-SEP-2000; 2000US-23577P.

25-SEP-2000; 2000US-235134P.

25-SEP-2000; 2000US-235134P.

26-SEP-2000; 2000US-2353134P.

26-SEP-2000; 2000US-235334P.
                                                                                     2000US-235711P.
2000US-235720P.
2000US-235840P.
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Weaver Z;
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stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
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Sequence 1023 BP; 312 Α, 244 ç; 240 G; 227 T; 0 other;

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                                                        sapiens
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h; lung; prostate; pancreas; carcinoma; antitumour; cancero
atic; gene therapy; antineoplastic; Wilm's tumour; adenocar
                                                                                                                 related gene sequence
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adenocarcinoma, cancerous; ö

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The present invention describes a method (M1) for screening for an anti-neoplastic agent. The method involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, determining a change in expression of at least one gene (I) of a signature gene set, where (I) comprises a sequence (S) selected from 847 sequences (given in ABL61664 to ABL70110), or is at least 95% identical to (S), where a change in expression is indicative of anti-neoplastic activity. (I) has cytostatic activity and can be used in gene therapy. MI can be used for screening an anti-neoplastic agent, and can be used for producing a product which is the data collected with respect to the anti-neoplastic agent as a structure and/or properties of the agent. MI can be used in the structure and/or properties of the agent. MI can be used in the treatment of cancer such as colon, breast, stomach, lung, thyroid, adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's tumour.
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2000US-237604P.
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Weaver Z;
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20-SEP-2000;
22-SEP-2000;
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27-SEP-2000;
27-SEP-2000;
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27-SEP-2000;
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Soppet DR,
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                                                   .
0
                        Length 1023;
                       Score 527; DB 24; Length 1
Pred. No. 2.2e-156;
0; Mismatches 80; Indels
Sequence 1023 BP; 312 A; 244 C; 240 G; 227 T; 0 other;
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71..98
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                       78.5%;
87.8%;
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                                                 Matches 575, Conservative
                                      Similarity
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                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                            bronchitts, pneumonia, bronchiectasis, emphysema, asthma, tuberculosis or fungal infections. It can also be used for adjunctive treatment of abscesses or severe closed-space infections in conditions such as empyema, meningitis, peritonitis, sinusitis, otilis, periodontitis, septic arthritis, as well as in topical treatments in a variety of inflammatory and infected lesions, e.g. of the skin and mucosal membranes, surgical wounds, ulcerative lesions and burns. LS-DNase may improve the efficacy of antibiotics used in the treatment of such infections (e.g. gentamicin activity is markedly reduced by reversible binding to intact DNA). It can also be used for the treatment of other con-infected conditions in which there is an accumulation of cellular Cdebris that includes cellular DNA, such as pyelonephritis and conditions to assays of a viscous material (e.g. sputum) from a patient. The anti-LS-DNase antibodies can be used for detection and purification of of LS-DNase antibodies can be used for detection and purification.
                                                                                                                                                                                                                                                                                                                            Query Match
Best Local (
                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA-containing material, as well as treatment of systemic lupus erythematosus or pulmonary disease of disorders such as certaining material.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated LS-DNase which is resistant to inhibition by used for the treatment of e.g systemic lupus erythematosus pulmonary diseases and disorders such as cystic fibrosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA sequence encodes a novel human LS-DNase (AAW23542),
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 CTGCTGTCAAAGACTTCGTGATTATCCCCCCTGCACACCACCCCAGAGACATCCGTTAAGG
                        CCGCTGTCAAGGACTTCGTGATTGTCCCCCCTGCACACCCCCCTGAGACATCCGTTAGAG
                                                             ATGGAGACGCAGATGTTTTTCCAGGGAGCCCTTTGTGGTCTGGTTCCAATCTCCCCACA
                                                                               CTGGAGACGCAGATGTGTTTTCCAGGGAACCCTTTGTGGTCTGGTTCCAGTCACCCTACA
                                                                                                                         TTCTCTACAAGGAAAAGCTGGTGTCTGTGAAGAGGGAGTTATCACTACCATGACTATCAGG
                                                                                                                                             TTCTCTATAAAGAAAAGCTAGTGTCTGTAAAACAAAGCTACCTCTACCACGACTATCAGG
                                                                                                                                                                                       CGTACAACTATGTGATTAGCTCTCGGCTTGGAAGAACACATATAAAGAACAATATGCCT
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                                                                                                                                                                                                                                                                                                                             Similarity
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/product= LS-DNase
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87.8%;
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                                                                                                             Detecting granulocyte activation by detecting dif
of genes associated with granulocyte activation,
diagnostic markers that is useful for monitoring
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                                                                                                                                                                                                                                                                                                                                                                        granulocyte activation;
                                                                                                                                                                                                                                                                                                                                                                                    adult respiratory distress syndrome; inflammatory bowel disconn's disease; ulcerative colitis; periodontal disease;.
                                                                                                                                                                                                                                                                                                                                                                                                            rheumatoid arthritis; glomerulonephritis; asthma; thrombosis; cardiac reperfusion injury; renal reperfusion injury; ARDS;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; ss; granulocytic cell; DNA chip; bacterial infection; viral infection; parasitic infection; protozoal infection; fungal infection; sterile inflammatory disease; psoriasis;
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disease state
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The invention relates to detecting (M1) granulocyte (GC) active (GCA), by detecting the level of expression of gene(s) (Gs) iddinated the chip analysis as given in the specification, and comparing the expression level to an expression level in an unactivated GC, where differential expression of Gs is indicative of GCA.

Claim 1;

SEQ ID No 1000; 114pp;

English

activation

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CC that alters the expression of at least one gene in Gs; (2) screening (M3) (for an agent capable of modulating GGA or an inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease using the control in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease, by detecting the chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease, by detecting the chronic) in a tissue, an allergic response in a subject, exposure of gene (s) from Gs, where the level of expression of the gene is indicative of inflammation; or in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease, by contacting a tissue having or sterile inflammatory disease, by contacting a tissue having or sterile inflammatory disease, by contacting an agent capable of modulating GA preferably in an inflammation in a tissue; M4 is useful for modulating GA, M3 is useful for secrening an agent capable of modulating correcting an inflammation (sepcially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease (e.g. psoriasis, rheumatoid arthritis, creptiusion injury, ARDS, adult respiratory distress syndrome, inflammatory bowel disease, Crohn's disease, ulcerative colitis, periodontal disease, also bacterial infection, viral infection and M5 is useful for treating one of the above conditions. The present correction, but was obtained in electronic for the printed specification, but was obtained in electronic for the printed specification, but was obtained in electronic for the printed specification, but was obtained in electronic
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Pred. No. 7.5e-156;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   81; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1108 BP; 329 A; 261 C; 271 G; 247 T; 0 other;
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Matches 574; Conservative
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07-APR-2000; 2000US-195225P. 09-APR-2001; 2001WO-US10802

18-OCT-2001

(ZHAN/) ZHANG H M. (AXRL/) AX R L. Zhang HM, Ax RL; WPI; 2002-066307/09.

P-PSDB; AAU11517

480 CGGTCAAGAAGAGCACAAACTGCGCCTATGACAGGATCGTGCTTAGAGGACAAAATATTG 540 CCGCTGTCAAGGACTTCGTGATTGTCCCCCTGCACACCACCCTGAGACATCCGTTAGAG 300 AGATTGATGAGCTGGCTGATGTCTACACAGATGTGAAACGTCGCTGGAATGCAGAGAATT 360 TCATTTTCATGGGTGACTTCAATGCTGGCTGCAGCTACGTCCCCAAGAAGGCCTGGAAGG 420 AGATCGATGAGTTGAGGTCTACACGGACGTGAAACACCCCTGGAAGGCGGAGAATT 642 643 TCATTITICATGGGTGACTICAATGCCGGCTGCAGCTACGTCCCCAAGAAGGCCTGGAAGA 702 ACATCCCCTTGAGGACTGACCCCAGGTTTGTTTGGCTGATCGGGGACCAAGAGGACACCA 762 CTGCTGTCAAAGACTTCGTGATTATCCCCCTGCACCACCACCCCCAGAGACATCCGTTAAGG ACATCCGCCTGAGGACGGACCCCAAGTTCGTTTGGCTGATCGGGGACCAAGAGGACACCA 703 523 583 301 421 241 361 481 ò g ò g 8 g g ò a ò ò

763 CGGTGAAGAAGCACCAACTGTGCATATGACAGGATTGTGCTTAGAGGACAAGAAATCG 822

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Fertility-associated antigen, FAA; antiinfertility, sperm cell acrosome, reproductive fitness; single nucleotide polymorphism; SNP; human;
600
                 823 TCAGTICTGTTGTTCCCAAGTCAAACAGTGTTTTTGACTTCCAGAAAGCTTACAAGCTGA 882
                                                                                                                                              Partail cDNA encoding human fertility-associated antigen (FAA), HC1
TCAACTCTGGTGGTCCTCAATCAAACCTCGTCTTTGATTTCCAGAAAGCTTACAGGTTGT
                                  655
                                          883 CTGAAGAGGGCCCTGGATGTCAGCGACCACTTTCCAGTTGAATTTAAACTACA 937
                                                                                                                                                                                                                                                                    /note= "No start or stop codon given"
/transl_except= (pos:1..3, aa:KVIKRCDIILVMEIKDS)
/transl_except= (pos: 253..255, aa:S)
                                  CTGAATCGAAGGCCCTGGATGTCAGCGACCACTTTCCAGTTCATCATCATCATCA
                                                                                                                                                                                                                                                    "Human fertility-associated antigen,
                                                                                                                                                                                                                                           "Human FAA"
                                                                                                                                                                                                                  Location/Qualifiers
                                                                                           AAS17901 standard; cDNA; 556 BP
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                                                                                                                                                                                                                                          product=
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                                                                                                                                                                                                  Homo sapiens.
                                                                                                                             26-MAR-2002
                                                                                                            AAS17901;
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The invention describes a novel isolated human fertility-associated antigen (FAA) and a bovine FAA polypeptide. Human or bovine FAA is useful for increasing the stability of a sperm cell acrosome and for increasing the by administering FAA. Detecting single the fertility of a human male by administering FAA. Detecting single incleotide polymorphisms (SNPs) of the human or bovine FAA gene is useful consaaying fertility by detecting the presence or absence of a FAA SNP in the mammal. The FAA SNPs are chosen from FAA SNPs 1-34 given in the specification. FAA SNP is also useful for determining the reproductive fitness of a human or bovine, by determining the nucleotide sequence of the FAA SNP and correlating the fertility of more than one mammal containing the FAA SNP and correlating the fertility of more than one mammal containing the FAA SNP and correlating the ferquency of the FAA SNP to the ceproductive fitness of the mammals. FAA improves the integrity of sperm membranes and increases the capacitation of sperm derived from either fertile or infertile humans. Barly genetic identification of infertility in mproves the prognosis for subsequent attempts at fertilisation and Novel human or bovine fertility-associated antigen useful for stabilising sperm cell acrosome and increasing fertility of a male Claim 1; Fig 2A-E; 54pp; English.

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RESULT 11
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ID AAT1773
XX AAT17
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                                                                                                                                                  Deoxyribonuclease; DNase-gammma; selective cleavage; linker; chromatin DNA; cell nucleus; 3'-hydroxy; 5'-phosphate; apoptosis; carcinogenesis; AIDS development; diagnosis; prevention; creatment; cancer; autoimmune disease; viral infections; ds.
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1.5e-154;
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Best Local S
Matches 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence encodes the deoxyribonuclease, DNase-gammma, which is able to selectively cleave the linker part of chromatin DNA. DNase-gamma has a mol. wt. of 32000 by SDS-PAGE, or 30000 by gel filtration, an optimum pH of 5.6, is found in the cell nucleus, is not dependent on divalent cations, has a Zn(2+) inhibition IC(50) > ImM and leaves 3'-OH and 5'-P termini after cleavage. The DNase can be used at a mol. level to resolve the control mechanisms of carcinogenesis, the autoimmune system and AIDS development. It can also be used in the diagnosis, prevention and treatment of cancer, autoimmune disease, viral infections, etc., and as an apoptosis control agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNase which selectively cuts linker region of useful in diagnosis, treatment and prevention diseases, viral infections, etc.
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                ACATCCGCCTGAGGACGGACCCCAAGTTCGTTTTGGCTGATCGGGGACCAAGAGGACACCA
                                                                                                                                 AGATTGATGAGCTGGCTGATGTCTACACAGATGTGAAACGTCGCTGGAATTGCAGAGAATT
                                                                                                                                                                                         CCGCTGTCAAGGACTTCGTGATTGTCCCCCTGCACACCACCCCTGAGACATCCGTTAGAG
                                                                                                                                                                                                                               ATGGAGACACAGACGTGTTTTCCAGGGAGCCCTTTGTGGTTTGGTTCCAGGCGCCCTTCA
                                                                                                                                                                                                                                                  CTGGAGACGCAGATGTGTTTTCCAGGGAACCCTTTGTGGTCTGGTTCCAGTCACCCCTACA
                                                                                                                                                                                                                                                                                      TCCTCTACAAGGAGAAGCTGGTGTCTGTGAAGGCAAAATACCTCTACCATGACTATCAGG
                                                                                                                                                                                                                                                                                                           TTCTCTATAAAAGAAAAGCTAGTGTCTGTAAAACAAAGCTACCTCTACCACGACTATCAGG
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                                                                                                                                                                                                                                                                                                                                                                CATACAACTATGTGATTAGCTCTCGCCTTGGAAGAAACACATATAAAGAACAGTATGCCT
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                                                                      TCATTTTCATGGGTGACTTCAATGCTGGCTGCAGCTACGTCCCCAAGAAGGCCTGGAAGG
                                                                                                                                                                        CTGCTGCCAAGGACTTCGTGATTGTCCCCCTTGCACACTCCTGAAACCTCTGTTAAAG
ACATCCGTTTGAGGACAGACCCCAACTTTGTTTGGCTGATTGGGGACCAAGAGGACACCA
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                    CGGTCAAGAAGAGCACAAACTGCGCCTATGACAGGATCGTGCTTAGAGGACAAATATTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNase; actin; DNA viscoelasticity; systemic lupus erythematosus; cystic fibrosis; meningitis; pulmonary disease; gene therapy; recombinant preparation; DNA-hydrolytic activity; ss.
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                                                                                                                                                                                                                                               CTGAATCGAAGGCCCTG---GATGTCAGCGACCACTTTCCAGTTCA
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248..1105
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/product= LS-DNase
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                    in in
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treatment of such infections (e.g. gentamicin activity is markedly reduced by reversible binding to intact DNA). It can also be used in vitro diagnostic assays of a viscous material (e.g. sputum) from a patient. The anti-LS-DNase antibodies can be used for detection and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      partial cDNA encoding human fertility-associated antigen (FAA), HC2.
                                                                                                                                                                                                                                                                                                                                                       TCTCTATAAAGAAAAGCTAGTGTCTGTAAAACAAAGCTACCTCTACCACGACTATCAGGC
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                                                                                                                                                                                                                                                                                   ATACAACTATGTGATTAGCTCTCGCCTTGGAAGAAACACATATAAAGAACAGTATGCCTT
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                                                                                                                                          DB 18; Length 1124;
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                                                                                                                                       70.8%; Score 474.8; DB 18; Length 82.9%; Pred. No. 8.2e-140; ive 0; Mismatches 112; Indels
                                                                                                      Sequence 1124 BP; 299 A; 273 C; 273 G; 279 T; 0 other;
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                                                                       purification of LS-DNase.
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                                                                                                                                                                         Matches 542;
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The invention describes a novel isolated human fertility-associated antigen (FAA) and a bovine FAA polypeptide. Human or bovine FAA is useful for increasing the stability of a sperm cell acrosome and for increasing the fertility of a human male by administering FAA. Detecting single curve fertility of a human male by administering FAA. Detecting single for assaying fertility by detecting the presence or absence of a FAA SNP in the mammal and correlating the presence or absence with the fertility of the mammal. The FAA SNPs are chosen from FAA SNPs 1-34 given in the specification. FAA SNP is also useful for determining the reproductive finness of a human or bovine, by determining the mucleotide sequence of the FAA SNP, quantifying the fertility of more than one mammal containing the FAA SNP and correlating the frequency of the FAA SNP to the membranes and increases the capacitation of sperm derived from either fertile or infertile humans. Early genetic identification and facilitates early intervention to determine whether the individual may facility for the fertility from the fertilisation and
                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local
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P-PSDB; AAU11518.
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                                                                                                                                                                                                                                                                                                                                         CAGGGAACCCTTTGTGGTCTGGTTCCAGTCACCCTACACCGCTGTCAAGGACTTCGTGAT 262
                                                                                                                                   CTACACAGATGTGAAACGTCGCTGGAATGCAGAGAATTTCATTTTCATGGGTGACTTCAA
                                                                                                                                                                                                                                        CAGGGAACCCTTTGTGGTCTGGTTCCAGTCACCCCTACACCGCTGTCAAGGACTTCGTGAT 60
                             349;
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AX R L.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the novel FAA gene
                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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/note= "
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                                                                                                                                                                                                                                                                                                                                                                                                                                       51.9%;
99.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                                                                                            Score 348.4; DB 24
Pred. No. 5.1e-100;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  described in the method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93 G;
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nucleotide polymorphisms (SNPs) of the human or bovine FAA gene is useful for assaying fertility by detecting the presence or absence of a FAA SNP in the mammal and correlating the presence or absence with the fertility of the mammal. The FAA SNPs are chosen from FAA SNPs 1-34 given in the specification. FAA SNP is also useful for determining the reproductive fitness of a human or bovine, by determining the nucleotide sequence of the FAA SNP, quantifying the fertility of more than one mammal containing reproductive fitness of the mammals. FAA improves the integrity of sperm membranes and increases the capacitation of sperm derived from either fertile or infertile humans. Early genetic identification of infertility improves the prognosis for subsequent attempts at fertilisation and facilitates early intervention to determine whether the individual may benefit from fertility treatments to avoid costly and/or emotional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  reproductive HC3; ss.
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                                                                                                                                                                                                                                                                                                                                      Claim 1; Fig 2A-E; 54pp; English.
                                                                                                                                                                                                                                                                                                                                                                       Novel human or bovine fertility-associated antigen useful stabilising sperm cell acrosome and increasing fertility of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zhang HM,
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(AXRL/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fertility-associated antigen; FAA; antiinfertility; sperm cell acrosome; reproductive fitness; single nucleotide polymorphism; SNP; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         partial cDNA encoding human fertility-associated antigen (FAA),
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AX R L.
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/transl_except= (pos:251..253, aa: Arg)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note= "Human fertility associated antigen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 product= "Human FAA"
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AX RL;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fertility-associated antigen; FAA; antiinfertility; sperm cell acrosome; reproductive fitness; single nuclectide polymorphism; SNP; human; HC4; ss.
problems with attempted inseminations. This sequence encodes the human fertility-associated antigen (FAA), HC3, one of 4 partial prostate CDNA clones of the novel FAA gene described in the method of the invention.
                                                                                                                                                            120
                                                                                                                                                                              CTACACAGATGTGAAACGTCGCTGGAATGCAGAGAATTTCATTTTCATGGGTGACTTCAA 382
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                                                                                                203 CAGGGAACCCTTTGTGGTCTGGTTCCAGTCACCCTACACGCTGTCAAGGACTTCGTGAT 262
                                                                                                                                        CAAGTICGITITGGCTGATCGGGGACCAAGAGGACACCACGGTCAAGAAGAGCACAAACTG 502
                                                                                                                                                                                                                                                                              241 CAAGTTCGTTTGGCTGATCGGGGACCAAGAGGACACCACGGTCAAGAAGAGAAGAACTG 300
                                                                                Gaps
                                                                                                              Partial cDNA encoding human fertility-associated antigen (FAA), HC4.
                                                                                                                                                          TATCCCCTGCACACCCCCAGAGACATCCGTTAAGGAGATCGATGAGTTGAGTTGAGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "No start or stop codon given"
/trans1 except= (pos: 11..12, aa:Phe)
/note= "This codon has an apparent 1 nucleotide
deletion which alters the reading frame"
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/note= "Human fertility-associated antigen, HC4'
                                                           Score 314.8; DB 24; Length 350;
Pred. No. 2.3e-89;
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                                                                               0; Mismatches 22; Indels
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                                         Sequence 350 BP; 89 A; 93 C; 94 G; 74 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                     AAS17904 standard; cDNA; 349
                                                         Query Match
Best Local Similarity 93.7%;
Matches 328; Conservative
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(AXRL/) AX R L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            fitness of a human or bovine, by determining the nucleotide sequence of the FAA SNP, quantifying the fertility of more than one mammal containing the FAA SNP and correlating the frequency of the FAA SNP to the reproductive fitness of the mammals. FAA improves the integrity of sperm membranes and increases the capacitation of sperm derived from either fertile or infertile humans. Early genetic identification of infertility improves the prognosis for subsequent attempts at fertilisation and facilitates early intervention to determine whether the individual may benefit from fertility treatments to avoid costly and/or emotional problems with attempted inseminations. This sequence encodes the human fertility-associated antigen (FAA), HC4, one of 4 partial prostate cDNA clones of the novel FAA gene described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               206 GGAACCCTTTGTGGTCTGGTTCCAGTCACCCTACACGCTGTCAAGGACTTCGTGATTGT 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CACAGATGTGAAACGTCGCTGGAATGCAGAGATTTCATTTTCATGGGTGACTTCAATGC 385
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 GGGAGCCCTTGTGGTCTGGTTCCAATCTCCCCACACTGCTGTCAAAGACTTCGTGATTAT 62
                                                                                                              Novel human or bovine fertility-associated antigen useful for stabilising sperm cell acrosome and increasing fertility of a male
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .;
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Pred. No. 7.3e-85;
0; Mismatches 29
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                                                                                                                                                                                                                                 Claim 1; Fig 2A-E; 54pp; English
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91.6%;
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Matches 318; Conservative
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Job time : 201.384 secs
WPI; 2002-066307/09.
P-PSDB; AAU11520.
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Title: Perfect score:

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Scoring table:

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Minimum DB Maximum DB

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Contact: Genoscope

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

BP 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr.

Location/Qualifiers

location/Qualifiers

/db_xref="texon:9606"
/clone="CSODIO26YK08"
/clone="CSODIO26YK08"
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/clone="CSODIO26YK08"
/clone="Diacentra"
/lissue Lype="placentra"
/note="Vector: pCMVSPORT 6; Site_1: Not1; 1st strand cDNA
was primed with a Not1-oligo(dT) primer. Five prime end
                                     B1460950 603207187
AW543802 C0174C07-
AW543802 C0174C07-
AW915564 EST7346868
B18138188 603083104
B1660448 We67C07.x
B1833952 603083104
B0710632 AGENCOURT
AW538998 C0115F01-
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AW241180 xn29e10.x
BF33166 602028119
AW43180 xn29e10.x
BF33166 60203047
AM43430 L114C04.x
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AM803005 IL2-UM007
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AA989198 cq95d05.s
H78110 yu84a11.r1
AW827162 xn06e10.y
BM386137 UI-R-CN1-
                              BG530136 602558626
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1 (bases 1 to 890)

Li,W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished (2001)
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AA989198
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Query Match Best Local Sim Matches 576;

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                                                                                                                                                             prime, mF
AL546432
    Eukaryota; Metazoa;
Mammalia; Eutheria;
1 (bases 1 to 896)
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                                                                                                                                          GI:12879540
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| CTGAATCGAAGGCCCTGGATGTCAGCGACCACTTTCCAGTTCATCATCATCATCATCA
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                                                                                                              TCAACTCTGGTGGTCCTCAATCAAACCTCGTCTTTGATTTCCAGAAAGCTTACAGGTTGT
                                                                                                                                                               CGGTGAAGAAGAGCACCAACTGTGCATATGACAGGATTGTGCTTAGAGGACAAGAAATCG
                                                                                                                                                                                                                                                                                                                                            TCATTTTCATGGGTGACTTCAATGCCGGCTGCAGCTACGTCCCCAAGAAGGCCCTGGAAGA
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BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Li,W.B., Gruber,C., Jessee,
Full-length cDNA libraries
Unpublished (2001)
Contact: Genoscope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     h 78.5%;
Similarity 87.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:9606"
/clone="CSODIO30YD20"
/clone_1ib="LTI_NFL006_PL2"
/clone_lib="LTI_NFL006_PL2"
/tissue_type="placenta"
/note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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oraries and normalization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 526.6; DB 9;
Pred. No. 1.6e-140;
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SOURCE ORGANISM

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ACCESSION DEFINITION

REFERENCE

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/organism="Homo sapiens"
/db xref="taxon:9606"
/clone="csollo268K08"
/clone="csollo268K08"
/clone="type="pIacenta"
/tissue_type="pIacenta"
/rote="wector: pCWNSPORT 6; Site_1: NotI; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies. Contact: Feng Liang Life Technologies. Rockville, Maryland 20850, USA Fax: (1) 301 610 8371
Email: fliangelifetech.com URL: http://fulllength.invitrogen.com; 7 others
                                                                                                                                                                                                                                                                                                                                                                                                                          833 bp mRNA linear EST 16-FEB-2001
ALS72037 LTI_NFL006_PL2 Homo sapiens cDNA clone CSODI026YK08 3
ALS72037
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Fill-length cDNA libraries and normalization
Contact: Genoscope
                                                                                                                                                         272 CGGTGAAGAAGAGCACCAACTGTGCATATAACAGGATTGTGCTTAGAGGACAAGAAATCG 213
                                                                                                                                                                                                                     TCAACTCTGGGGGCCTCAATCAAACCTCGTCTTTGATTTCCAGAAAGCTTACAGGTTGT 600
                                                                                                                                                                                                                                               392 TCATTITCATGGGTGACTICAATGCCGGCTGCAGCTCCCCAAGAAGGCCTGGAAGA 333
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BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
_Location/Qualifiers
                                                                                      332 ACATCCGCTTGAGAACTGACCCCAGGTTTGTTTGCTGATCGGGGACCAAGAGACAA
                                                                                                                                CGGTCAAGAAGAGCACAAACTGCGCCTATGACAGGATCGTGCTTAGAGGACAAATATTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 TTCTCTATAAAGAAAAGCTAGTGTCTGTAAAACAAAGCTACCTCTACCACGACTATCAGG
                                                                                                                                                                                                                                                                                                       CTGAATCGAAGGCCCTGGATGTCAGCGACCACTTTCCAGTTCATCATCATCATCA 655
                                                                                                                                                                                                                                                                                                                             CTGAAGAGGGCCCTGGATGTCAGCGACCACTTTCCAGTTGAATTTAAACTACA 98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 511; DB 9; I
Pred. No. 4.8e-136;
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86.9%;
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Best Local Similarity
Matches 570; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     human.
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AL572037/c
LOCUS
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KEYWORDS
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/clone lib="LTINEDGE PL2"
/tissue_type="placenta"
/note="Vector: pcwVspORT 6; Site_l: NotI; lst strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pcwVspORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com"

Ntb://fulllength.invitrogen.com"
7 others
                                                                                                        AL571894 LTI_NFL006_PL2 Homo sapiens cDNA clone CSODI030YD20 3
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                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 931)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CATACAACTATGTGATTAGCTCTCGCCTTGGAAGAACACATATAAAGAACAGTATGCCT 120
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BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
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840 CTGAAGAGGCCCCTGGATGTCAGCGACCACTTTYCAGTTGAATTTAAACTACA 894
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Pred. No. 2.9e-138;
2; Mismatches 85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CSODI030YD20"
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86.7%;
                                                                                                                                              prime, mRNA sequence.
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AV607154.1
EST.
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Shirakawa Institute of Animal Genetics
Odakura, Nishigo, Nishi-shirakawa, Fukushima
Tel: 81-248-25-5641
                                                                                                                                                                                                                                                                                                                          and Sugimoto,Y.

Establishment of a high throughput EST sequencing system using poly(A) tail-removed cDNA libraries and determination of 36,000
                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora;
Bovidae; Bovinae; Bos.
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3', mRNA sequence.
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Nucleic Acids Res. 29 (22),
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                                                                                                                 le pass sequencing.
clone was obtained from
Location/Qualifiers
                                                                                                                                                                 kazusugi@cocoa.ocn.ne
/organism="Bos taurus"
/db_xref="taxon:9913"
/clone="EIKI039B05"
/clone_lib="Bos taurus k
/tissue_type="kidney"
/dev_stage="fetus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  BE048177 666 bp mRNA linear EST 20-OCT-2000 tz46h09.yl NCI_CGAP_Brn52 Homo sapiens cDNA clone IMAGE:2291681 5'similar to SW:DHP2_HUMAN Q13609 DNASE I HOMOLOGOUS PROTEIN DHP2
                                                                                                                          Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D.,
R. Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                  Mammalia; Eutheria; Primates; Catarrhini; Hominidae (bases 1 to 666)
NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.National Cancer Institute / National Institute of N Disorders and Stroke, Brain Tumor Genome Anatomy Pr
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL, send email to:
info@image.llnl.gov
Insert Length: 1048 Std Error: 0.00
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Unpublished (1998)
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Mammalia; Eutheria;
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/note="Vector: pZL1; Site_1: %
/mas deleted from a Not1 site"
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97.7%;
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1 (bases 1 to 642)
Tanaka,T.S., Jaradat,S.A., Lim,M.K., Kargul,G.J., Wang,X., Grahovac,M.J. Panteno,S., Sano,Y., Piao,Y., Nagaraja,R., Doi,H., Wood,W.H. III, Becker,K.G. and Ko,M.S.H.
Genome-wide expression profilling of mid-gestation placenta and embryo using a 15,000 mouse developmental cDNA microarray Proc. Natl. Acad. Sci. U.S.A. 97 (16), 9127-9132 (2000)
                        Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                              Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@lgsun.grc.nia.nih.gov
Plate: C0168 row: H column: 07
Seq primer: -21M13 Forward
High quality sequence stop: 642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1. .642
/organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                               Contact: George J. Kargul
                                                                                                                                                                                                                                                                                                                                                                                                                                   POLYA=Yes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ..
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                                                                                                                                                                                                            /note=Torgan: brain; Vector: pCMV-SPORT6; Site 1: Sall; Site 2: Not1; This library represents the normalized version of NoT CGAP Brn35. Cloned unidirectionally. Primer: Oligo dr. Average insert size 1:19 kb. Tumor types include: meningioma, oligodendroglioma, astrocytoma (grade II), medulloblastoma, astrocytoma (grade IV).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 CATACAACTATGTGATTAGCTCTCGCCTTGGAAGAAACACATATAAAGAACAGTATGCCT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TICICIATAAAGAAAAGCTAGIGICIGIAAAACAAAGCTACCICIACCACGACTATCAGG 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGATCGATCAGTTGGTTGAGGTCTACACGGACGTGAAACACCGCTGGAAGGCGGAGAATT 454
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                                                                                                      /db_xref="taxon:9606"
/clone="IMAGE:2291681"
/clone=lib="NCI_CGAP_Brn52"
/tisuse=type="tumor, 5 pooled (see description)"
/lab_host="DH108"
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                                                                                                                                                                                                                                                                                                                                                                     2 others
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                                                                                      /organism="Homo sapiens"
Seg primer: -40kr 11000 High quality sequence stop: 431.
Location/Qualifiers
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/note="Vector: pSPORT1 (Gibco/BRL Life Technology);
Site 1: Sal1; Site 2: Not1; Total RNAs were extracted from 5 EPC. The double-stranded cDNA was synthesized by Gibco's kit with an Oligo(dT) primer [Not1 primer-adapter from GibcoBRL]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                 /clone_lib="NIA Mouse E7.5 Extraembryonic Portion cDNA
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              /db_xref="niaEST:C0168H07-3"
/db_xref="taxon:10090"
                                                                                                                /dev_stage="7.5dpc_Embryo"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              148 g
/strain="C57BL/6J
                                               /clone="C0168H07"
                                                                                                    /sex="unknown"
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                                                                                    Library
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BI522352.1 GI
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NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies,
                                                                                                                                                                                                                                                                                                                                                       Plate: LLAM11554
                                                                                                                                                                                                                                                                                                                                                                       http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                         found through the I.M.A.G.E. Consortium/LLNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nman
                                                                                                                                                                                                                                                                                       quality sequence start: 18 quality sequence stop: 695.
Location/Qualifiers
/note="Organ: pooled pancreas and spleen; Vector: pCMV-SPORT6; Site 1: Not1; Site 2: ECORV (destroyed); RNA source anonymous pool of spleen and pancreas from 28 yo male. Library is oligo-dT primed and directionally cloned (ECORV site is destroyed upon cloning). Average insert size 1.5 kb, insert size range 1-2.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 025. Note: this is a NIH_MGC Library."
                                                                                                                                                                              /lab
                                                                                                                                                                                        /db_xref="taxon:9606"
/clone="IMAGE:5220532"
/clone_lib="NIH_MGC_120"
                                                                                                                                                                                                                                                     organism="Homo sapiens
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                                                                                                                                                                                                                                                              mRNA sequence.
BG867772
BG867772.1 GI
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium
DNA Sequencing by: Incyre Genomics, Inc.
Clone distribution: MGC clone distribution informat
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                            NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
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                                                                                                      /organism="Mus musculus"
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/db_xref="texon:10090"
/clone="ImAGE=1912893"
/clone="ImB-MCI CGAP_SG2"
/lab_most="DH10B (TI_phage=resistant)"
/note="Organ: salivary gland; Vector: pCMV-SPORT6; Site 1:
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е
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Plate: LLAM10817 row: e column:
High quality sequence stop: 799.
Location/Qualifiers
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825 bp mRNA linear EST 03-APR-2001 Homo sapiens cDNA clone IMAGE:4696638 5',

BG530136 602558626F1 NIH_MGC_61 mRNA sequence. BG530136 BG530136.1 GI:13521673

DEFINITION

ACCESSION VERSION

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="InMAGE:4696638"
/clone="InMAGE:4696638"
/clone="InMIN MGC_61"
/tissue_type="embryonal carcinoma"
/tissue_type="embryonal carcinoma"
/lab host="InHI MGC_61"
/note="Organ: testis; Vector: pDNR-LIB (Clontech); Site_1:
Sfil (ggccgcctcggcc); Site_2: Sfil (ggccattatggcc);
Double-stranded cDNA was prepared from cell line RNA. 5'
and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-CACGCCATATGGCC-3' and 3' adaptor
sequence: 5'-ATTCTACAGGCCCAGGCCGCACATG-dT(30)BN-3'
(where B = A, C, or G and N = A, C, Or T). Average
insert size 1.75 kb (range 0.9-4.0 kb). 15/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA). Note: this is a NIH_MGC
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ن
Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 825)
NIH-MGC http://mgc.nci.nih.gov/.
NIH-MGC lttp://mgc.nci.nih.gov/.
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                     Email: cgapbs-remail.nih.gov
Tissue Procurement: ATC
CDNA Library Preparation: CLONETECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1524 row: c column: 07
High quality sequence stop: 743.
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ACAACAGGATCTGCCCCATACTGATGGAGAAGCTGAACAGAAATTCAAGGAGAGGCATAA 199
                       ACAACAGGATCTGCCCCATACTGGATGGAGAAGCTAAACGGAAATTCAAGAAAAGGCATAA 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tissue Procurement: Miklos Palkovits, M.D., Ph.D. CDNA Library Preparation: Michael J. Brownstein (Nt Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                603207187F1 NIH MGC 97 Homo sapiens cDNA clone IMAGE:5272917
                                                                                                                                                                                                                                                                                                                                                                                 High quality sequence stop: 628.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D Email: cgapbs-r@mail.nih.gov
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                                                                                                                                                                                                                                                                                                                                                                                                                              found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
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                                                                                                                                        181
                                                            61.9%; llarity 90.6%; Conservative
                                                                                                                                        α
                                                                                                                                   /note="Organ: testis; Vector: pBluescriptR (modified pBluescript KS+); Site 1: BamHI; Site 2: Sall-XhoI (gtcgag); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTTTTVN-3', size-selected for average insert size 2.2 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Captrapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                          /clone="IMAGE:5272917"
/clone_lib="NIH_MGC_97"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                   organism="Homo sapiens"
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Pred. No. 1.5e-108;
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1 (bases 1 to 620)
Tanaka, T.S. Jaradat, S.A., Lim, M.K., Kargul, G.J., Wang, X., Grah, M.J., Pantano, S., Sano, Y., Piao, Y., Nagaraja, R., Doi, H., Wood, III, Becker, K.G. and Ko, M.S.H.
Genome-wide expression profiling of mid-gestation placenta and embryo using a 15,000 mouse developmental cDNA microarray Proc. Natl. Acad. Sci. U.S.A. 97 (16), 9127-9132 (2000)
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                                                                                                                                                                                                                                                                                                                                                    Email: cdna@lgsun.grc.nia.nih.gov
Plate: C0174 row: C column: 07
Seq primer: -21M13 Forward
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National Institute on Aging/National Institutes of Health
National Drive, Suite 4000, Baltimore, MD 21224-6820, USA
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AW543802
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                                                                                                                                                                                                                                                                                                                      quality sequence stop:
Library"
                                                            /db_xref="niaEST:C0174C07-3"
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                                                                                                                                                             organism="Mus musculus"
|strain="C57BL/6J"
                                 /clone_lib="NIA Mouse
                                                                                                                                                                                                                                                              location/Qualifiers
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82.1%; Pred. No. 1.2e-107;
iive 0; Mismatches 103; Indels 0;
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/dev_stage="7.5dpc_Embryo"
/lab_host="DH108"
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RESULT 13 AI927844/c

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/note="Organ: kidney, Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not 1; Site 2: Eco RI; Plasmid DNA from the normalized library NCI CGAP Kid3 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDS 1322376-1323911, 1456007-1456775, and 1500552-1502855). Subtraction by Bento Soares and M. Patima Bonaldo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
EST 08-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                        wo91g09.xl NCI CGAP Kid11 Homo sapiens cDNA clone IMAGE:2462752 3' similar to SW:DHP2 HUMAN Q13609 DNASE I HOMOLOGOUS PROTEIN DHP2 PRECURSOR ;, mRNA sequence.
                                                                                                                                                                                                                                                                 Euteleostomi;
                                                                                                                                                                                                                               Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 784)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  488
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGTGACTTCAATGCTGGCTGCAGCTACGTCCCCAAGAAGGCCTGGAAGGACATCCGCCTG 431
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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   linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  73; Indels
   mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 739 Std Error: 0.00
Seg primer: -40UP from Gibco
High quality sequence stop: 426.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1. .784
/organism="Homo sapiens"
/db_xref="Laxon:9666"
/clone="IMAGE:2462752"
/clone_lib="NCI_CGAP_Kidll"
/lab_host="DH10E"
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   784 bp
                                                                                                                 AI927844
AI927844.1 GI:5663808
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Matches 451; Conservative
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Unpublished (1997)
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AW540389/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 610)
1 (bases 1 to 610)
Tanaka, T.S., Jaradat, S.A., Lim, M.K., Kargul, G.J., Wang, X., Grahov,
M.J., Pantano, S., Sano, Y., Piao, Y., Nagaraja, R., Doi, H., Wood, W.,
III, Becker, K.G. and Ko, M.S.H.
Genome-wide expression profiling of mid-gestation placenta and
embryo using a 15,000 mouse developmental cDNA microarray
Proc. Natl. Acad. Sci. U.S.A. 97 (16), 9127-9132 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Laboratory of Genetics
National Institutes of Health
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdnaelgsun.grc.nia.nih.gov
Plate: C0132 row: C column: 04
Seq primer: -21M13 Forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AW540389 610 bp mRNA linear ES C0132C04-3 NIA Mouse E7.5 Extraembryonic Portion cDNA musculus cDNA clone C0132C04 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: George J. Kargul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AW540389
AW540389.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       quality sequence stop: 610
/note="Vector: pSPORT1 (Gibco/BRL Life Technology); Site_1: Sall; Site_2: NotI; Total RNAs were extracted from SEPC. The double-stranded cDNA was synthesized by Gibco's kit with an Oligo(dT) primer [NotI primer-adapter]
                                                                                                                                                                                                                                    from GibcoBRL
                                                                                                                                                                                                                                                                                                                                             /dev_stage="7.5dpc Embryo'
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                 Library'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                            sex="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          strain="C57BL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                      clone_lib="NIA Mouse E7.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                        clone="C0132C04"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             xref="niaEST:C0132C04-3"
_xref="taxon:10090"
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Wood,W.H.
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                                                                                                                                                                                                          AW915564
                                                                                                                                                                                                                       RESULT 15
                                                                                                                                                                                               LOCUS
          TITLE
                                    AUTHORS
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Best Local
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                                                                                                                                                                                                                                                                                      CCACTTTCCAGTTCATCATCATCATCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACCCTTTGTGGTCTGGTTCCAGTCACCCCTACACCGCTGTCAAGGACTTCGTGATTGTCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGGAAGAAACACATATAAAGAACAGTATGCCTTTCTCTATAAAGAAAAGCTAGTGTCTGT 148
                                                                                                                                                                                                                                                                                                                                 CGTCTTTGATTTCCAGAAAGCTTACAGGTTGTCTGAATCGAAGGCCCTGGATGTCAGCGA
                                                                                                                                                                                                                                                                                                                                                                                                                    TGTTTGGCTGATTGGGGACCAAGAGGACACTACGGTCAAGAAGAGTACCAGCTGTGCCTA
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                                                                                                                                                           EST346868 Normalized rat embryo, RGICW80 5' end, mRNA sequence.
                                                                                                  Rattus sp.
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          Rat Genome Project:
                       Lee, N.H., Glodek, A., Chandra, I., Kerlavage, A.R. and Adams, M.D.
                                  Lee, N.H.,
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Contact: Lee, NH

The Institute for Genomic Research
9712, Medical Center Drive, Rockville, MD 20850, USA
9713, Modical Center Drive, Rockville, MD 20850, USA
9714, Modical Center Drive, Rockville, MD 20850, USA
9715, Modical Center Drive, Rockville, MD 20850, USA
Fax: (301)-838-0208

Email: nhlee@tigr.org
This clone is available through the ATCC, contact the ATCC
tel#703-55-5700 for Lurther information
Seq primer: M13 Reverse.
Location/Qualifiers
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GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.	OM nucleic - nucleic search, using sw model	Run on: December 9, 2002, 08:59:53 ; Search time 40.9082 Seconds (without alignments) 5030.295 Million cell updates/sec	Title: Verfect score: 671 Sequence: 1 acaacaggatctgccccataatcatcatgaagaaccatga 671	Scoring table: IDENTITY_NUC Gapop 10.0 , Gapext 1.0	Searched: 441362 seqs, 153338381 residues	Total number of hits satisfying chosen parameters: 882724	Minimum DB seq length: 0 Maximum DB seq length: 200000000	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	<pre>Database : Issued Patents NA:* 1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:* 2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:* 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:* 4: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:* 5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:* 6: /cgn2_6/ptodata/1/ina/bcTUS_comB.seq:*</pre>	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	SUMMARIES	ery tch Length DB ID Descript:	481.2 71.7 1208 1 US-08-640-765A-2 481.2 71.7 1208 3 US-09-073-613-2 163.2 24.3 1039 1 US-07-895-300A-2	163.2 24.3 1039 4 US-09-638-112-2 Sequence 163.2 24.3 1039 5 PCT-US93-05136-2 Sequence 163.2 24.3 1039 5 PCT-US93-05136-2 Sequence	161.6 24.1 1039 1 US-08-458-367-2 Sequence 124.6 18.6 1615 2 US-08-491-988-15 Sequence	9 124.6 18.6 1624 2 US-08-491-988-14 Sequence 1 124.6 18.6 1648 2 US-08-491-988-13 Sequence	1 119 17.7 1055 2 US-08-468-012A-1 Sequence 2 119 17.7 1055 4 US-09-054-989-1 Sequence 3 35.2 5.2 1427 3 US-09-173-581-10 Sequence	1 35.2 5.2 1427 4 US-09-420-915-10 Sequence 2 32.8 4.9 1293 2 US-08-924-440-1 Sequence 3 3.2 4.8 289 4 US-09-0707-005-17 Sequence	3.2.2 4.8 7289 4 US-09-244-796-17 Sequence 3.3.2 4.8 7218 1 US-08-232-463-14 Sequence	20 31.0 4.7 1511 2 05-08-505-763-3 Sequence 21 31.8 4.7 1511 3 US-08-956-253-3 Sequence 21 31 6 4 7 1511 4 IS-08-956-253-90 Sequence	31.2 4.6 248 3 US-08-513-974B-300 Sequence 3 31.2 4.6 248 3 US-08-513-974B-301 Sequence	24 30.6 4.6 1920 1 US-08-487-753-1 Sequence 1, Appli 25 30.6 4.6 1920 2 US-08-480-065-1 Sequence 1, Appli 26 30.6 4.6 1920 3 US-08-487-744-1 Sequence 1, Appli 27 30.6 4.6 1920 5 PCT-US93-09167-1 Sequence 1, Appli

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Patent No. 6143875
GENERAL INFORMATION:
APPLICATION NUMBER: US
FILING DATE: 06-MAY-11
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 01
                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                    APPLICANT: Tanuma, Sei-ichi
TITLE OF INVENTION: ANTIBOD
NUMBER OF SEQUENCES: 12
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REFERENCE/DOCKET NUMBER: 851
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 616-5600
TELEPAX: (312) 616-5700
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1108 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        71.7%;
Hest Local Similarity 85.1%;
Matches 550; Conservative
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FILING DATE: 06-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: LARCHER, Carol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
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                       CTGAATCGAAGGCCCTG---GATGTCAGCGACCACTTTCCAGTTCA
                                                                   TCAACTCTGTGGTTCCCCGCTCCAGTGGCGTCTTTGACTTTCAGAAAGCTTATGAGTTGT
                                                                                                      TCAACTCTGGTGGTCCTCAATCAAACCTCGTCTTTGATTTCCAGAAAGCTTACAGGTTGT
                                                                                                                                             CGGTCAAGAAGAGCACCAGCTGTGCCTATGACAGGATTGTCGTTCGCGGACAAGAGATAG
                                                                                                                                                                                CGGTCAAGAAGAGCACAAACTGCGCCTATGACAGGATCGTGCTTAGAGGACAAAATATTG
                                                                                                                                                                                                                       ACATCCGTTTGAGGACAGACCCCAACTTTGTTTGGCTGATTGGGGACCAAGAGGACACCA
                                                                                                                                                                                                                                                           ACATCCGCCTGAGGACGGACCCCAAGTTCGTTTGGCTGATCGGGGACCAAGAGGACACCA
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Pred. No. 5.8e-139;
0; Mismatches 93;
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477 ACCACGGTCAAGAAGACCACAAACTGCGCCTATGACAGGATCGTGCTTAGAGGACAAAAT 536
                                                     829 ACCACAG --- CTACACCCACGCACTGTGCCTATGACAGGATCGTGGTTGCAGGGATGCTG 885
                                                                                                                                                             886 CTCCGAGGGGCGTTGTTCCCGACTCGGCTCTTCCCTTTAACTTCCAGGCTGCCTATGGC 945
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                                                                                                           537 ATTGTCAACTCTGGTGGTCCTCAATCAAACCTCGTCTTTGATTTCCAGAAAGCTTACAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genetech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Frenz, John
APPLICANT: Shire, Steven J.
APPLICANT: Shire, Steven J.
APPLICANT: Sliwkowski, Mary B.
TITLE OF INVENTION: PURIFIED FORMS OF DNase
CORRESPONDENCES: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/09/638,112
FILING DATE: 09-Aug-2000
                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/09638112
Patent No. 6440412
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Johnston, Sean A. REGISTRATION NUMBER: 35,910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 1039 base pairs TYPE: Nucleic Acid STRANDEDNESS: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: POTELECOMMUNICATION INFORMATION TELEPHONE: 650/225-3562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Generatech, Inc. STREET: 1 DNA Way CITY: South San Francisco STATE: California COUNTRY: USA
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Best Local Similarity
Matches 335; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     769 TCATCCATCCGCCTGTGGACAAGCCCCACCTTCCAGTGGCTGATCCCCGACAGCGCTGAC 828
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches 243;
GENERAL INFORMATION:
APPLICANT: Frenz, John
APPLICANT: Shire, Steven J.
APPLICANT: Shire, Steven J.
APPLICANT: Shiwkowski, Mary B.
TITLE OF INVENTION: PURIFIED FORMS OF DNase
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: Culifornia
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/895,300A
FILING DATE: 19920608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27,043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 74
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 19920608
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 1039 bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Hensley, Max D. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: NUCLEIC ACID
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                              ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
Matches 335; Conserve
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US-07-895-300A-2
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RESULT 5
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                                         PCT-US93-05136-2
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APPLICANT: Genentech, Inc.
 Query Match
                                                                                                                                 TELEPHONE: 415/225-3562
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: 5.25 inch, 360 Kb |
COMPUTER: IBM PC compatible |
OPERATING SYSTEM: PC-DOS/MS-DOS |
SOFTWARE: patin (Genentech) |
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: 5.25 inv
                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
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                                                                                                                                                                                                                                                   NAME: Johnston, Sean A.
REGISTRATION NUMBER: P35,910
REFERENCE/DOCKET NUMBER: 747
                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: FILING DATE: 19930
                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 460 Point San Bruno
CITY: South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                 LENGTH:
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                                                                                                                   1039 bases
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Genentech, Inc.
TVENTION: PURIFIED FORMS OF DNase
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                                                         ss: single
linear
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   24.3%;
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 Score 163.2;
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Length 1039;
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GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
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                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Genentech, Inc.
TITLE OF INVENTION: Compact
TITLE OF INVENTION: Therapy
UNMBER OF SEQUENCES: 1
                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
                                                                                                                         SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
ATTORNEY/AGENT INFORMATION:
                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS: ADDRESSEE: Genentech,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              237
                                                                                                                                           COMPUTER: IBM PC OPERATING SYSTEM: SOFTWARE: patin
                                                                                     APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                     STREET: 460 Point San Bruno
CITY: South San Francisco
                    FILING DATE:
                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAGGCTGGAGACGCAGATGTGTTTTCCAGGGAACCCTTTGTGGTCTGGTTCCAGTCACCC 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTCGTGTACAGGCCTGACCAGGTGTCTGCCGTGGACAGCTACTACGATGATGGCTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACATACAACTATGTGATTAGCTCTCGCCTTGGAAGAACACATATAAAGAACAGTATGCC 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACCACAG----CTACACCCACGCACTGTGCCTATGACAGGATCGTGGTTGCAGGGATGCTG
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                                                                                                                                                                                                                                       94080
                                                                                                                                                                                                                                                                      California
                                                                                                                                                                                                                                                     USA
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                                                                                                                                                        IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                                                                        PCT/US93/10519
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Johnston, Sean

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60 ACATACAACTATGTGATTAGCTCTCGCCTTGGAAGAAACACATATAAAGAACAGTATGCC 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   469 ricgiciacacecreaceacárcicieceaceacáciaciaciaciaciaciacarcarcace 528
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 161.6; DB 1; Length 1039;
Pred. No. 3e-40;
0; Mismatches 244; Indels 6;
                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                   OPEKATING STSTEM: PC-DOS/MS-DOS SOCTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA: US08/458,367
APPLICATION NUMBER: US/08/458,367
FILING DATE: O2-Jun-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/409631
FILING DATE: 22-Mar-1995
PRIOR APPLICATION NUMBER: 08/348284
FILING DATE: 30-No. 578433-1994
PRIOR APPLICATION NUMBER: 08/116186
FILING DATE: 02-Sep-1993
PRIOR APPLICATION NUMBER: 08/116186
FILING DATE: 02-Sep-1993
PRIOR APPLICATION NUMBER: 08/116186
FILING DATE: 02-Sep-1993
APPLICATION NUMBER: 08/116186
FILING DATE: 08-Sun-1992
APPLICATION NUMBER: 08/116186
FILING DATE: 08-Sun-1992
APPLICATION NUMBER: 07/895300
FILING DATE: 08-Jun-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Johnston, Sean A.
REGISTRATION NUMBER: 35,910
REPERENCE/POCKET NUMBER: P0747C4
TRIECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-3562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 1039 base pairs TYPE: Mucleic Acid STRANDEDNESS: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
24.1%;
Best Local Similarity 57.2%;
Matches 334; Conservative
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            California
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US-08-458-367-2
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                                                                                                                                                                                                                                                                                                                                                   24.3%; Score 163.2; DB 5; Length 1039; ilarity 57.4%; Pred. No. 9.5e-41; Conservative 0; Mismatches 243; Indels 6;
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Sequence 2, Application US/08458367

Patent No. 2783433

GENERAL INFORMATION:

APPLICANT: Frenz, John

APPLICANT: Shire, Steven J.

APPLICANT: Slinkowski, Mary B.

TITLE OF INVENTION: PURIFIED FORMS OF DNA

NUMBER OF SEQUENCES: 18

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 460 Point San Bruno Blvd

CITY: South San Francisco
REGISTRATION NUMBER: 35,910
REFERENCE/DOCKET NUMBER: 792C;
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/925-3562
TELEFAX: 415/952-9881.
TELEFX: 910/371-7168
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISITES:
LENGTH: 1039 bases
                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
PCT-US93-10519-1
                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                   Matches 335;
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                                                                                                                                                                                                                                                                                                                                                                               Local
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                                                                                                                                                                                                                                                                                                                                                                                                         US-08-491-988-15
                                                                                                                                                                                                                                                                                                                       Best Local Similarity 53.7 Matches 312; Conservative
                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 15, Application US/08491988 Patent No. 5973116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: EPENETOS, AGAMEMNON A.
APPLICANT: SPOONER, ROBERT A.
APPLICANT: DEONARAIN, WAHENDRA
TITLE OF INVENTION: Compounds for targeting
NUMBER OF SEQUENCES: 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 212-818-9479
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PALENTIN Release #1.0, Version
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
1189
                                                                                                                                                                                                                                         1009
                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: 212-986-4090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: MCAULAY NISSEN GOLDBERG KIEL & HAND, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                 120
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FILING DATE: 18-DEC-1995
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: GOLDBERG, JULES REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ENGTH:
TCTACCAAGGTTAAAGAGTTCGCTATCGTTGCTCTGCACAGCGCGCCCGTCTGACGCTGTT 1248
                                                                                                                                                                                                                                                                                 ACATACAACTATGTGATTAGCTCTCGCCTTGGAAGAAACACATATAAAGAACAGTATGCC 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTGAGTGACCAACTGGCCCAAGCCATCAGTGACCACTATCCAGT 989
                                   TACACCGCTGTCAAGGACTTCGTGATTGTCCCCCTGCACACCACCCCTGAGACATCCGTT 296
                                                                           GAATCTTGCGGTAACGACTCTTTCTCCCGGGAACCGGCTGTTGTTAAATTCTCGAGCCAC 1188
                                                                                                                   CAGGCTGGAGACGCAGATGTGTTTTCCAGGGAACCCTTTGTGGTCTGGTTCCAGTCACCC 236
                                                                                                                                                                                               TTTCTCTATAAAGAAAAGCTAGTGTCTGTAAAACAAAGCTACCTCTACCACGAC---TAT 176
                                                                                                                                                                                                                                       ACCTACCACTACGTTGTTTCTGAACCCCTCGGGCGTAACTCTTACAAAGAACGGTACCTG 1068
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Pred. No. 1e-28
0; Mismatches
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RESULT 9
US-08-491-988-14
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                                                                               US-08-491-988-14
   Matches 312;
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                   Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 14,
                                                                                                                                                                                                     TELEFAX: 212-818-9479
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: EPENETOS, AGAMEMNO
APPLICANT: SPOONER, ROBERT A.
APPLICANT: DEONARAIN, MAHENDR
TITLE OF INVENTION: Compounds
                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                              NAME: GOLDBERG, JULES E.
REGISTRATION NUMBER: 24,408
TELECOMMULICATION INFORMATION:
TELEPHONE: 212-986-4090
                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/491,988
                                                                                             MOLECULE TYPE: HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1486
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1546 CTTTCGAACGAAATGGCGCTGGCCATCTCTGATCACTACCCGGTTGA 1592
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FILING DATE: 18-DEC
CLASSIFICATION: 424
                                                                                                                                 TOPOLOGY:
                                                                                                                                               STRANDEDNESS:
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                                                                                                                                                                                      ENGTH:
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                     Similarity
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   Conservative
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Score 124.6; DE Pred. No. 1e-28; 0; Mismatches 2
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                                  DB 2;
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Gaps
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SEQUENCE CHARACTERISTICS
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                                                         TITCTCTCTATAAAGAAAAGCTAGTGTCTGTAAAACAAAGCTACCTCTACCACGAC---TAT 176
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| Patent No. 5973116
| GENERAL INFORMATION:
| APPLICANT: SPONER, ROBERT A. |
| APPLICANT: DEONARAIN, MAHENDRA |
| TITLE OF INVENTION: Compounds for targeting |
| NUMBER OF SEQUENCES: 29 |
| CORRESPONDENCE ADDRESS: |
| ADDRESSEE: MCAULAY NISSEN GOLDBERG KIEL & HAND, LLP |
| STREET: 261 MADISON AVENUE |
| CITY: NEW YORK
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/491,988
FILING DATE: 18-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 10016-2391
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: GOLDBERG, JULES E.
REGISTRATION UNURBER: 24,408
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-986-4099
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INFORMATION FOR SEQ ID NO: 13:
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US-08-491-988-13
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                                                                                                                                                                                                                                 Length 1648
                                                                                                                                                                                                                           Query Match 18.6%; Score 124.6; DB 2; Length Best Local Similarity 53.2%; Pred. No. 1e-28; Matches 312; Conservative 0; Mismatches 269; Indels
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APPLICANT: RUBEN, ET AL.
TITLE OF INVENTION: Human DNase
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/08468012A
Patent No. 5830744
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LENGTH: 1648 base pairs
TYPE: nucleic acid
                                                         single
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MEDIUM TYPE: 3.5 INC
COMPUTER: IBM PS/2
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NEW JERSEY
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                                          STRANDEDNESS:
TOPOLOGY: line
MOLECULE TYPE: C
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US-08-468-012A-1
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Sequence 1, Application US/09054989
Patent No. 6251648
GENERAL INFORMATION:
APPLICANT: RUBEN, ET AL.
TITLE OF INVENTION: Human DNase
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                              RESULT 12
US-09-054-989-1
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: PCT/US94/04954
FILING DATE: 5 MAY 1994
ATTORNEY/AGENT INFORMATION:
NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33,073
REGISTRATION NUMBER: 32,5500,442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: LI
MOLECULE TYPE:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
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SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/-
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TELEPHONE: 201-994-1744
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les 252; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: NUCLEIC ACID
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CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI, STEWART & OLSTEIN
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Best Local Similarity 55.4%;
Matches 252; Conservative
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CLASSIFICATION:
PRIOR APPLICATION UNMBER: 08/468
APPLICATION NUMBER: 08/468
FILING DATE: 6-JUNE-1995
APPLICATION NUMBER: PCT/US
APPLICATION NUMBER: PCT/US
FILING DATE: 5 MAY 1994
ATTORNEY/AGENT INFORMATION:
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TOPOLOGY: LIN:
MOLECULE TYPE:
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STATE: "-
COUNTRY: USF
COUNTRY: 07068
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CURRENT APPLICATION DATA:
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CITY: R
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM:
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 GAGGAGGCCCTCAACATCAGTGACCACTACCCCGT
                               TCGAAGGCCCTGGATGTCAGCGACCACTTTCCAGT
                                                                                                 TCTGGTGGTCCTCAATCAAACCTCGTCTTTGATTTCCAGAAAGCTTACAGGTTGTCTGAA 605
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                                                                   CGGAGTCTGCTGCACACTGCGGCTGCCTTTGACTTCCCCACGAGCTTCCAGCTCACCGAG
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HERSEY
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                                                                                                                                   857 AATGCAGATAAGATCAAGATCAAGATCGCAGACCTGGCCAACGCCTGCTGGGTGCACAAG 916
                                                                                                                                                                               408 AAGGCCTGGAAGGACATCCGCCTGAGGACGGACCCCAAGTTCGTTTGGCTGATCGGGGAC 467
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                                                                                         Length 1427;
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5.2%; Score 35.2; DB 4; Length 153.7%; Pred. No. 0.39; ive 0; Mismatches 63; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Frits et al.
TITLE OF INVENTION: MUTANT THERMONOSPORA SPP. CELLULASE
NUMBER OF SEQUENCES:
ADDRESSEE: Genenoor International, Inc.
STREET: 925 Page Mill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       42; Indels
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OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/924,440
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Pred. No. 2.1;
0; Mismatches
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                         US-08-924-440-1
; Sequence 1, Application US/08924440
; Patent No. 5871550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Christopher L. Stone
REGISTRATION NUMBER: 35,696
REFERENCE/DOCKET NUMBER: GC3E
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 846-7555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 58.0%;
Matches 58; Conservative
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1293 base pairs
Query Match
Best Local Similarity 53.74
Matches 73; Conservative
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MEDIUM TYPE: Diskette
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STRANDEDNESS: single
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APPLICANT: Frits
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STATE: CA
COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1427;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; DB 3;
0.39;
                                                                                                                       APPLICANT: Vie, Henry
APPLICANT: Guegler, Karl J.
APPLICANT: Gorley, Neil C.
APPLICANT: Gorley, Neil C.
APPLICANT: Azimzai, Yalda
APPLICANT: Azimzai, Yalda
APPLICANT: Azimzai, Yalda
APPLICANT: Lu, Aina
TITLE OF INVENTION: Protein Kinase Homologs
FILE REFERENCE: PF-0614 US
CURRENT APPLICATION NUMBER: US/09/173,581A
CURRENT FILING DATE: 1998-10-15
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PERL PROGram
SEQ ID NO 10
TENTION OF 10
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APPLICANT: Guegler, Karl J.
APPLICANT: Gorgone, Gina
APPLICANT: Gorgone, Gina
APPLICANT: Azimaai, Yalda
APPLICANT: Azimaai, Yalda
APPLICANT: Azimaai, Yalda
APPLICANT: Lu, Aina
TILE DE INVENTION: Protein Kinase Homologs
FILE REFERENCE: PF-0614 US
CURRENT APPLICATION UNMER: US/09/420, 915
CURRENT FILLING DATE: 1999-10-20
EARLIER APPLICATION NUMBER: US 09/173, 581
BARLIER FILLING DATE: 1998-10-15
NUMBER OF SEO ID NOS: 18
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Patent No. 6264947
GENERAL INFORMATION:
                                                               APPLICANT: Bandman, Olga
APPLICANT: Tang, Y. Tom
APPLICANT: Hillman, Jennifer L.
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APPLICANT: Hillman, Jennifer L.
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US-09-420-915-10
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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Sequence 10, Applicat
Patent No. 6013455
GENERAL INFORMATION:
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/ Ggn2_6/ptodata/1/pubna/PCT_NEW_PUB.seq:*
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Compugen Ltd
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US-09-804-07-3392

US-10-133-065-1

US-10-074-509-1

US-10-133-065-1

US-10-134-065-11

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Maximum Match 100%
Listing first 45 summaries
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Sequence 3, Application US/09905114

Sequence 3, Application US/09905114

Patent No. US20020048745A1

GENERAL INFORMATION:

APPLICANT: ZHANG, HUANMIN

APPLICANT: AX, ROY L

APPLICANT: BELLIN, MARY E

TITLE OF INVENTION: ISOLATED POLYNUCLEOTIDE SEQUENCES ENCODING A FERTILITY ASSOCIATED

CURRENT APPLICATION NUMBER: US/09/905,114

PRIOR APPLICATION NUMBER: US 60/218,140

PRIOR PILING DATE: 2000-07-14

NUMBER OF SEQ ID NOS: 9

SEQ ID NOS: 9

SEQ ID NO 3

LENGTH: 671
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US-09-825-012-37
US-09-825-012-64
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CTGGAGACGCAGATGTGTTTCCAGGGAACCCTTGTGGTCTGGTTCCAGTCACCCTACA

121 TTCTCTATAAAGAAAAGCTAGTGTCTGTAAAACAAAGCTACCTCTACCACGACTATCAGG 180

TTCTCTATAAAGAAAAGCTAGTCTGTAAAACAAAGCTACCTCTACCACGACTATCAGG

121

61 CATACAACTATGTGATTAGCTCTCGCCTTGGAAGAAACACATATAAAAGAACAGTATGCCT

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US-09-905-114-1
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                                                                                                                                                                                                                    , NAME/KEY: CDS
; LOCATION: (1)..(59
; OTHER INFORMATION:
US-09-905-114-1
                                                                                                                                                                                                                                                                                                                                                APPLICANT: BELLIN, MARY E
TITLE OF INVENTION: ISOLATED POLYNUCLEOTIDE SE
FILE REFERENCE: 210707US20
CURRENT APPLICATION NUMBER: US/09/905,114
CURRENT FILING DATE: 2001-07-14
PRIOR APPLICATION UMBER: US 60/218,140
PRIOR FILING DATE: 2000-07-14
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin version 3.1
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                                                                                                                                                            Query Match
Best Local Similarity
Matches 592; Conserv
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Patent No. US20020048745A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 1
                                                                                                                                                                                                                                                                             LENGTH: 592
TYPE: DNA
ORGANISM: Bos sp.
FEATURE:
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APPLICANT: AX, ROY L
                   147
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GTAAAACAAAGCTACCTCTACCACGACTATCAGGCTGGAGACGCAGATGTGTTTTCCAGG
                                                                                                      GAGAAGCTAAACGGAAATTCAAGAAAAGGCATAACATACAACTATGTGATTAGCTCTCGC
                                                               CTTGGAAGAAACACATATAAAGAACAGTATGCCTTTCTCTATAAAGAAAAGCTAGTGTCT 146
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                                                                                                                                                                          88.2%; Score 592; DB 10; 100.0%; Pred. No. 3.1e-180;
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                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCES
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                                                                                                                                                                                       Length 592;
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GENERAL INFORMATION:
APPLICANT: SOMBET, Daniel
FITLE OF INVENTION: Cancer Gene Determination
FITLE OF INVENTION: Sets
FILE REFERENCE: 689290-75
CURRENT APPLICATION NUMBER: US/09/962,436
CURRENT FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: US/60/235,082
PRIOR APPLICATION NUMBER: US/60/234,924
PRIOR FILING DATE: 2000-09-25
PRIOR FILING DATE: 2000-09-25
                                                                                                                                                                                                                                                                                                                                                             ; LENGTH: 1023
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-962-436-336
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SOFTWARE: PatentIn version 3.0
SEQ ID NO 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 336, Application US/09962436 Patent No. US20020081301A1
                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 575; Conserv
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ATGGAGACGCAGATGTGTTTTCCAGGGAGCCCTTTGTGGTCTGGTTCCAATCTCCCCACA
                      CTGGAGACGCAGATGTGTTTTCCAGGGAACCCTTTGTGGTCTGGTTCCAGTCACCCCTACA
                                                                                          TTCTCTATAAAGAAAAGCTAGTGTCTGTAAAACAAAGCTACCTCTACCACGACTATCAGG
                                                                                                                                           CGTACAACTATGTGATTAGCTCTCGGCTTGGAAGAACACATATAAAGAACAATATGCCT
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                                                                   TTCTCTACAAGGAAAAGCTGGTGTCTGTGAAGAGGAGTTATCACTACCATGACTATCAGG
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                                                                                                                                                                                                                                                                                    Score 527; DB 10;
Pred. No. 3.4e-159;
0; Mismatches 80;
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                        215 ACAACAGGATCTGCCCCCATACTGATGGAGAGCTGAACAGAAATTCAAGGAGAGGCATAA 274
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                                                                                         CATACAACTATGTGATTAGCTCTCGCCTTGGAAGAACACATATAAAGAACAGTATGCT
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Patent No. US20020142981A1

GENERAL INFORMATION:

APPLICANT: Horne, Darci T.

APPLICANT: Scherf, Uwe

APPLICANT: Scherf, Uwe

APPLICANT: Gene Logic, Inc.

TILLE OF INVENTION: Gene Expression Profiles in Liver Cancer:

FILE REFERENCE: 44921-5028-WO

CURRENT APPLICATION NUMBER: US/09/880,107

CURRENT PAPLICATION NUMBER: US 60/211,379

PRIOR PILING DATE: 2000-66-14

PRIOR PLING DATE: 2000-10-02

PRIOR FILING DATE: 2000-10-02

NUMBER OF SEQ ID NOS: 3950

SOFTWARE: PatentIn Ver: 2.1

SEQ ID NO 3332

LENGTH: 1023
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ORGANISM: Homo sapiens
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| Patent No. US2002011507741
| Sequence 271, Application US/09954456
| Patent No. US2002011507741
| GRENEAL INCORMATION |
| APPLICANT: Young, Paul |
| TITLE OF INVENTION: Sets |
| FILE REFERENCE: 60920-76 |
| CURRENT FILING DATE: 2000-09-18 |
| PRIOR PALICATION NUMBER: US/60/234,052 |
| PRIOR PALICATION NUMBER: US/60/234,923 |
| PRIOR PALICATION NUMBER: US/60/235,134 |
| PRIOR PALICATION NUMBER: US/60/235,134 |
| PRIOR PALICATION NUMBER: US/60/235,638 |
| PRIOR PALING DATE: 2000-09-26 |
| PRIOR PALING DATE: 2000-09-27 |
| PRIOR PAL
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; ORGANISM: Homo sapiens
US-09-954-456-271
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US-09-954-456-271
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Sequence 1, Application US/10133065
Patent No. US20020123122A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                   Baron, Will F.
TITLE OF INVENTION: HUMAN DNASE
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb i
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/133,065
FILING DATE: 26-Apr-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Baker, Kevin
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                                                                                                                                                                                                    CITY: South San Francisco
STATE: California
COUNTRY: USA
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Best Local Similarity
Matches 575; Conserv
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SEQUENCE CHARACTERISTICS:
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TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID
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FILING DATE: 22/08/2000

APPLICATION NUMBER: 08/794827

FILING DATE: 04-Feb-1997

APPLICATION NUMBER: 60/109796

FILING DATE: 05-Feb-1996

APPLICATION NUMBER: 50/109796

ATTORNEY/ACENT INFORMATION:

NAME: Evans, David W

REGISTRATION NUMBER: *See attached Limited Recognition under 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: P1000R1C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1739
TELEFAX: GEOVICE
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                                                                                CTGAATCGAAGGCCCTGGATGTCAGCGACCACTTTCCAGTTCATCATCATCA
                                                                                                                                                                TCAACTCTGGTGGTCCTCAATCAAACCTCGTCTTTGATTTCCAGAAAGCTTACAGGTTGT
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                                                                                                                          TCAGTTCTGTTCCCCAAGTCAAACAGTGTTTTTGACTTCCAGAAAGCTTACAAGCTGA
                                                                                                                                                                                                      CGGTGAAGAAGAGCACCAACTGTGCATATGACAGGATTGTGCTTAGAGGACAAGAAATCG
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Pred. No. 3.5e-159;
O; Mismatches 80;
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NAME: Evans, David W REGISTRATION NUMBER: *See attached Limited Recognition under 37
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                                                                                                                                                   ACATCCGCCTGAGGACGCACCCCAAGTTCGTTTGGCTGATCGGGGACCAAGAGGACACCA
                                                                                                                                                                                                                                            CGGTCAAGAAGAGCACAAACTGCGCCTATGACAGGATCGTGCTTAGAGAGGACAAATATTG
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                                                                                                                                                                                                                                                                                                                                                                    801 TCAGTTCTGTTCTCCCAAGTCAAACAGTGTTTTTGACTTCCAGAAAGCTTACAAGCTGA
CTGAATCGAAGGCCCTGGATGTCAGCGACCACTTTCCAGTTCATCATCATCATCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTGAAGAGGAGGCCCTGGATGTCAGCGACCACTTTCCAGTTGAATTTAAACTACA 915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: 1BM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US.10/133,065
FILLING DATE: 26-Apr-2002
CLASSIFTCATION: cURNOWN>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C.F.R. 10.9 (b) REFERENCE/DOCKET NUMBER: P1000R1C3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 09/643,520
FILING DATE: 22/08/2000
APPLICATION NUMBER: 08/794827
FILING DATE: 04-Feb-1997
APPLICATION NUMBER: 60/10976
FILING DATE: 05-Feb-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TOPOLOGY: Linear SEQUENCE DESCRIPTION: SEQ ID NO: 11: US-10-133-065-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Baker, Kevin P.
Baron, Will F.
TITLE OF INVENTION: HUMAN DNASE
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
STREET: 1 DNA WAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 11, Application US/10133065
Patent No. US20020123122A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION TELEPHONE: 650/225-1739
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INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: Single
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COMPUTER READABLE FORM:
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87.8%; Pred. No. 3.5e-159;
tive 0; Mismatches 80; Indels
                                                                                                                                                                                                                                                                                                                                                           COMPUTER: 3.5 inch, 1.44 Mb floppy disk COMPUTER: 18M PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Windatin (Genetech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/074,509
FILING DATE: 11-Feb-2002
CLASSIFICATION NUMBER: 09/643,520
FILING DATE: 22/08/2000
FILING DATE: 22/08/2000
APPLICATION NUMBER: 08/794827
FILING DATE: 04-Feb-1997
APPLICATION NUMBER: 06/109796
FILING DATE: 05-Feb-1996
ATTORNEY/AGRRT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Johnston, Sean A.
REGIGTRATION NUMBER: 35,910
REFRENCE/CDOCKET NUMBER: P1000R1C2
TELECOMMUNICATION: INFORMATION:
TELEPHONE: 650/225-3562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                               Sequence 1, Application US/10074509; Patent No. US20020142437A1; GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
TITLE OF INVENTION: HUMAN DNASE
''NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                            ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
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                  US-10-074-509-1
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Best Local Similarity
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US-10-074-509-11
(S-10-074-509-11
; Sequence 11, Application US/10074509
; Patent No. US20020142437A1
; GENERAL INFORMATION:
COMPUTER READNELE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/074,509
FILING DATE: 11-Feb-2002
                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: HUMAN DNASE NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Baker, Kevin F. Baron, Will F.
                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                         CITY: South San F
STATE: California
                                                                                                                                                                                                                                                  ADDRESSEE: Genentech, STREET: 1 DNA Way
                                                                                                                                                                                        COUNTRY: USA
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Pred. No. 2.1e-142;
0; Mismatches 112;
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FILING DATE: 22/08/2000
APPLICATION NUMBER: 08/794827
FILING DATE: 04-Feb-1997
APPLICATION NUMBER: 60/199796
FILING DATE: 05-Feb-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62
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REFERENCE/DOCKET NUMBER: P10
TELECOMMUNICATION: INFORMATION:
TELEPHONE: 650/225-3562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 1124 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: <Unknown> PRIOR APPLICATION DATA:
                                                                                                                                                                CAACTCTGGTGGTCCTCAATCAAACCTCGTCTTTGATTTCCAGAAAAGCTTACAGGTTGTC
                                                                                                                                                                                                                                                                                                                    CATCCGCCTGAGGACCGCAAGTTCGTTTTGGCTGATCGGGGACCAAGAGGACACCAC
                                                                                                                                                                                                                                                                                                                                                                                                 CATTTTCATGGGTGACTTCAATGCTGGCTGCAGCTACGTCCCCAAGAAGGCCTGGAAGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATACAACTATGTGATTAGCTCTCGCCTTGGAAGAACACATATAAAGAACAGTATGCCTT 121
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                                        TGAGGAGGAGGCCCTGGATGTCAGTGATCACTTTCCAGTTGAGTTTAAGCTACA
                                                                                                                          CAACTCCGTGGTTCCCGGTTCCAGTGGCGTCTTTGACTTTCAGAAAGCTTATGACTTGTC
                                                                                                                                                                                                                                                  GGTCAAGAAGAGCACAAACTGCGCCTATGACAGGATCGTGCTTAGAGGACAAAATATTGT
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                                                                               TGAATCGAAGGCCCTGGATGTCAGCGACCACTTTCCAGTTCATCATCATCATCA
                                                                                                                                                                                                                                                                                        CATTCGTTTGAGGACGGACCCCAAGTTTGTTTGGCTGATTGGGGGACCAAGAGGACACTAC
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42; Conservative
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STRANDEDNESS: Single
TOPOLOGY: Linear
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Pred. No. 2.1e-142;
0; Mismatches 112;
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409 ACCTATCACTACGTGGTCAGTGAGCCACTGGGACGGAACAGCTATAAGGAGCGCTACCTG 468
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1039;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24.3%; Score 163.2; DB 10; Length 57.4%; Pred. No. 2.7e-42; Live 0; Mismatches 243; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 946 CTGAGTGACCAACTGGCCCAAGCCATCAGTGACCACTATCCAGT 989
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                                       US/09/771,078
                                                       FILING DATE:
CLASSIFICATION
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
TILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Glaister, Debra J.
REGISTRATION NUMBER: 33,888
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US-05-825-012-2
'Sequence 2, Application US/09825012
'Patent No. US20020122798A1
                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 792
TELECOMUNICATION INFORMATION:
TELEPHONE: 415/925-981
TELERX: 910/371-7168
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISICS:
LENGTH: 1039 bases
patin (Genentech)
                 CURRENT APPLICATION DATA APPLICATION NUMBER: US
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Matches 335, Conservative
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STRANDEDNESS: single
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29.2%; Score 195.6; DB 10; Length 392;
84.9%; Pred. No. 5.4e-53;
tive 0; Mismatches 39; Indels 0;
                              Sequence 630, Application US/09880107
Patent No. US20020142981A1
GENERAL INFORMATION:
APPLICANT: Horne, Joseph G.
APPLICANT: Scherf, Uwe
APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer FILE REPRENCE: 44921-5028-00.
CURRENT APPLICATION NUMBER: US/09/880,107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .us-09-77_-078-1
; Sequence 1, Application US/09771078
; Patent No. US2002034727A1
; GENERAL INFORMATION:
; APPLICANT: Mrsny, Randall J.,
; APPLICANT: Daugherty, Ann L.,
; APPLICANT: Daugherty, Ann L.,
; TITLE OF INVENTION: DNSSE W.;
; TOTALE OF INVENTION: DNSSE COMPACTION:
; CORRESPONDENCE ADDRESS:
; ADDRESSE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
CONTRY: USA
ZIP...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                PRIOR FILING DATE: 2000-06-14
PRIOR FILING DATE: 2000-06-14
PRIOR FILING DATE: 2000-06-14
PRIOR APPLICATION NUMBER: US 60/237,054
PRIOR FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 3950
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 630
LENGTH: 392
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ORGANISM: Homo sapiens
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; TYPE: DNA
; ORGANISM: Homo s
US-09-825-012-2
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US-09-825-012-4
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Sequence 4, Application US/09825012
Patent NO. US20020122798A1
GENERAL INFORMATION:
APPLICANT: Young, Robert
TITLE OF INVENTION: Compounds for Targeting
FILE REFERENCE: 43191-256808
CURRENT APPLICATION NUMBER: US/09/825,012
CURRENT FILING DATE: 2001-04-03
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APPLICANT: Young, Robert
TITLE OF INVENTION: Compounds for Targeting
FILE REFERENCE: 43191-256808
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Best Local
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CURRENT FILING DATE: 2001-04-03
PRIOR APPLICATION NUMBER: US 60/237,159
PRIOR FILING DATE: 2000-10-02
PRIOR APPLICATION NUMBER: GB 0008049.9
PRIOR FILING DATE: 2000-04-03
NUMBER OF SEQ ID NOS: 102
SOFTWARE: Patentin version 3.1
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Local Similarity 57.4%;
les 335; Conservative
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Pred. No. 2.7e-42;
0; Mismatches 243
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PRIOR APPLICATION NUMBER: US 60/237,159
PRIOR FILING DATE: 2000-10-02
PRIOR APPLICATION NUMBER: GB 0008049.9
PRIOR FILING DATE: 2000-04-03
NUMBER OF SEQ ID NOS: 102
SOFTWARE: Patentin version 3.1
SEQ ID NO 4
LENGTH: 783
RESULT 14
US-09-825-012-6
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                                                                                   TTGTCTGAATCGAAGGCCCTGGATGTCAGCGACCACTTTTCCAGT
                                                                  CTGAGTGACCAACTGGCCCAAGCCATCAGTGACCACTATCCAGT
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Similarity 57.2%;
34; Conservative
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Pred. No. 7.2e-42;
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FILE REFERENCE: 43191-256808

CURRENT APPLICATION NUMBER: US/09/825,012

CURRENT FILING DATE: 2001-04-03

PRIOR APPLICATION NUMBER: US 60/237,159

PRIOR FILING DATE: 2000-10-02

PRIOR APPLICATION NUMBER: GB 0008049.9

PRIOR FILING DATE: 2000-04-03

NUMBER OF SEQ ID NOS: 102

SOFTWARE: Patentin version 3.1

GENERAL

Sequence 6, Application US/09825012 Patent No. US20020122798A1

JENERAL INFORMATION:
APPLICANT: Young, Robert
TITLE OF INVENTION: Compounds for Targeting

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US-09-825-012-62
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                                                                                                   Length 858;
                                                                                            Query Match .24.1%; Score 161.6; DB 10; Length Best Local Similarity 57.2%; Pred. No. 7.6e-42; Matches 334; Conservative 0; Mismatches 244; Indels
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Patent No. US2002012798A1
GENERAL INFORMATION:
APPLICAMY: Young, Robert
TITLE OF INVENTION: Compounds for Targeting
FILE REPERCES: 43191-256608
CURRENT APPLICATION NUMBER: US/09/825,012
CURRENT FILING DATE: 2001-04-03
PRIOR PELLON DATE: 2000-02
PRIOR FILING DATE: 2000-02
PRIOR FILING DATE: 2000-06
PRIOR FILING DATE: 2000-06
PRIOR FILING DATE: 2000-06
PRIOR FILING DATE: 2000-06
SOFTWARE: Patentin Version 3.1
SEQ ID NO 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Artificial Sequence
                               TYPE: DNA
GORGANISM: Homo sapiens
US-09-825-012-6
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SEQ ID NO 6
LENGTH: 858
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                                                                                                                                                60 ACATACAACTATGTGATTAGCTCTCGCCTTGGAAGAAACACATATAAAGAACAGTATGCC 119
                                                                                                                                                                                                                                                                                            TITCICIATAAAGAAAAGCTAGTGTCTGTAAAAAAAAGCTACCTCTACCACGA---CTAT 176
                                                                                                                                                                                                                                                                                                                                                                                                                                 177 CAGGCTGGAGACGCAGATGTGTTTTCCAGGGAACCCTTTGTGGTTCGGTTCCAGTCACCC 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TACACCGCTGTCAAGGACTTCGTGATTGTCCCCCTGCACACCCCCTGAGACATCCGTT 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          297 AGAGAGATTGATGAGCTGGCTGATGTCTACACAGATGTGAAACGTCGCTGGAATGCAGAG 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AATTICATTITCATGGGTGACTICAATGCTGGCTGCAGCTACGTCCCCAAGAAGGCCTGG 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            417 AAGGACATCCGCCTGAGGACGGACCCCAAGTTCGTTTGGCTGATCGGGGACCAAGAGGAC 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACCACGGTCAAGAAGAGCACAAACTGCGCCTATGACAGGATCGTGCTTAGAGGACAAAAT 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  537 ATTGTCAACTCTGGTGGTCCTCAATCAAACCTCGTCTTTGATTTCCAGAAAGCTTACAGG 596
   Length 1548;
Score 161.6; DB 10; Length
Pred. No. 1.1e-41;
0; Mismatches 244; Indels
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Job time : 144.35 secs
   24.1%;
57.2%;
                                                                         Matches 334; Conservative
Query Match
Best Local Similarity
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